

899

```

1  ATGGACTTCA AACAAATTGA TTTTTCACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC TTAAGAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTTT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAAGAG CGGTGTTGAA AGCCGCCGCG GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWGH L AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTTCACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTCTGGTC GGGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAGATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAAGAG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWGHLEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPSNVVMGNSIVNRST					

```
|||||:
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDCLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:|||||:|||||:|||||:|||||:|||||:
g579-1  LPLCRAQVIVGVVDYNDCLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
          |||||:|||||:|||||:|||||:|||||:|||||:
g579-1  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

a579-1.seq

```
1  ATGGACTTCA AACAATTGGA TTTTTCACAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTTGGCGGT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACCCCTTG AGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

a579-1.pep

```
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPNSSV MGNSIVNRST LPLCRAQVIV GVDYNDCLKV
201 AKEAVLKAAY EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQORDIHI NS*
```

a579-1/m579-1 99.6% identity in 282 aa overlap

```
          10      20      30      40      50      60
a579-1.pep  MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1      MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1      VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1      GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep  LPLCRAQVIVGVVDYNDCLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:|||||:|||||:|||||:|||||:|||||:
m579-1      LPLCRAQVIVGVVDYNDCLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
```


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m579-1
 |||||
 AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
 51 cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
 101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
 151 tcgaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
 201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
 251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
 101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
 101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATCGGGCC GGTTCGGCA
 151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
 251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
 101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS					
g580	MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
 101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATCGGGCC GGTTCAGCA
 151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
 251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMASASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggtaaacc ggtatagaac aaaatacgtt
51 ctgtcgtcgt ggttttacc gcacgatat gggcggaat accgatgttg
101 cggtagagcg tgatcggggt cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgaagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggcttcgga cgcacatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgga acccaacgca ttgcaaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGN TDVAVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTACGAGCC ATTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTCTTCACG TTTTTC AAC GCACGCCAC GGCTTCGGA CGCATCAATC
251 AATTCGCTCG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGC
301 CGCATCGCA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGN TDVTVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGN TDVTVQADRG LTSHFISLSK LETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGN TDVAVQADRG LTSHFISLSK LETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG RINQFACQTQ VHGFLLTFAG RIANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAFG RINQLACQTQ IHGFLTTFAG RVANPTHQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMG	GNTDVT	VQADRG	LTSHFISLSK	LETEVRECFV	
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGG	NTDVT	VQADRG	LTSHFISLSK	LETEVRECFV	
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTF	FFQRTATAFG	RINQFACQTQ	VHGFLLTFAG	RIANPAHCQSQTAX
a581	GFSHTVYFFTF	FFQRTATAFG	RINQFACQTQ	VHGFLLTFAG	RIANPAHCQSQTAX
	70	80	90	100	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggacgggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggtt aagggcgagg cggctattgt tgttgaaaaa ggccggggatg
251 cgcttcctgc cgacagtgcg ggccgaaaccg ccgatattcta tacgcctttg
301 agcctgatgt acgacttgga caaaaacgat ttgcgcggcg tgttggcgct
351 acgcgaacac aatccgatgt accttatgcc gttttgggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cggtcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg ccgcatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcgat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcaaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc ggggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTSAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYDM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
 1 ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51 AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GGCAGGGGATG
251 CGCTTCTTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCTTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACATTCCGC
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCCGGACAG AGAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAG
501 CAAAATTGCC GAAGATTGT TTAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGGCGGAG TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAAATGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
 1 MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDVKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYDM GYGDVKLQYR
301 LNDRONVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYDMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYDMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582      LNDQRNVYSVLRYNPKTGYGAIEAAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTCT CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAAACCAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TTAAACCCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTCT GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGCG CCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLDKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHNKQNGIGI GLMFNDLDGI *

m582/a582  100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVRH
          |||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
               130      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYMGYGDVQLQYR
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIDYMGYGDVQLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               ||||||||||
a582          GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcect
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgctt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg caatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcagcg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRPSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTTCGAA AGAGCGAGAC TGTAAACGAT GCCACGCTT TTTCTTCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTORIAHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD
g583	MIIDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK	KQISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTORIAHR	RARFVGGYAG
g583	AQRFSKNGDK	KQISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTORIAHR	RARFVGGYAG
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLLDP	VGYGQCQNQG	AQYCGNGEGY
g583	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLLDP	VGYGQCQNQG	AQYCGNGEGY
	190	200				
m583.pep	RFETQFHHD	LKKDRPEKSEKX				
g583	RFETQFHHD	LKKDRPEKSEKX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAT TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACC CGGT TTGTGCGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTORIAHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNGSQQ	QFGKSETVTD

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAAARGIGRGNGSQQFGKSETVTD
              10      20      30      40      50      60

              70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
              |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
              70      80      90      100     110     120

              130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              130     140     150     160     170     180

              190     200
m583.pep  RFETQFHHIDLKKDRPEKSEKX
              |||||
a583      RFETQFHHIDLKKDRPEKSEKX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1   atgctgcgtt ctatcttggc ggcttcctctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggtctgg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgcggtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggtctg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtta cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:...

```

1   MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEPK AGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1   ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAATTCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGmAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAAG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

          10      20      30      40      50      60
m584.pep  MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
          ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAAEGRDKNVNA
          10      20      30      40      50      60

          70      80      90     100     110     120
m584.pep  EFVKKFNKFI RSKKNGSFKTELVSRSAMPRYQYTNRRRIQTGWEERAEFKVEGRDFDELN
          ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      EFVKKFNFT RSKKNGSFKTELVSRSAMPRYQYTNRRRIQTGWEERAEFKAEGRDFDALN
          70      80      90     100     110     120

          130     140     150     160     170     180
m584.pep  RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
          ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      RFIADVQDASLEDTFVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
          130     140     150     160     170     180

          190     200     210     220     230
m584.pep  NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
          ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      NFGQIGSHIAGDGAVRAKMLRAMPMAASVMKGTDSAAPGVEEISISINGTVQFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGT GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

          10      20      30      40      50      60
m584.pep  MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
          ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584      MLRSILAASL-----IVEFS ESAGVEAVQDTMSARFQVTAEGRDKNVNA
          10      20      30      40

```

```

              70      80      90      100      110      120
m584.pep      EFVKKFNKFIRKSKNGSFKTELVSRSAMPRIQYTNGRRIQTGWEEAEFKVEGRDFDELN
              |||||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           EFVKKFNNFTRKSKNGSFKTELVSRSAMPRIQYTNGRRIQTGWEEAEFKVEGRNFDALN
              50      60      70      80      90      100

              130      140      150      160      170      180
m584.pep      RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
              |||||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
              110      120      130      140      150      160

              190      200      210      220      230
m584.pep      NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX
              170      180      190      200      210      220
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt tccaacgcat tttcgccaca ttttgccgcg ttatcgctcg
51  cgcaatcttt gtggcgagtt tttctttttg gctgggtgcag aacacccttg
101 ccgaaaacca attcaaccaa cgccgcacca tcgaaaccac attgatgggc
151 agcattatgt ccgcattcaa gacacggggc gacaacggcg cgccgcgaat
201 cctgaccgaa tggaaaaaca gcccgcgttc atccgcggtt tacgtcatat
251 agggcgacga gaaaaaagac atcttaaacc gctatatcga caattacacc
301 atagaacgcg cccggctggt tgcgcgaac aacccccatt ccaaccttgt
351 ccgcatcgaa tacgaccgtt tcggcgaaga atacctgttc ttcattaaag
401 gctgggacaa ccaccaggca caacgcctgc ccagcccgct gtttateccg
451 ggcctgcccg ttgcccgat ttggcacgaa ttcattcatc tctccttcac
501 catcattgtc ggactgctga tggcatatat ccttgccggc aacattgcca
551 aacccatcag aatcttaggc aacggcatgg acagggtggc agaacgagaa
601 cttgaagacc gcgtttgccg acaggttcgc gaccgcgacg acgaattggc
651 cgatgttgcc atgcaattcg acacaatggt ggaaaaactg gaataa
```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGDDEKD ILNRYIDNYT
101 IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPLFIP
151 GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE
201 LEDRVCQQVR DRDDELADVA MQFDTMVEKL E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT TCCAACGCAT TTTGCCACA TTTTGCGCGG TTATCGTCTG
51  TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCCTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGCGGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGAACC GGTATATCGA CAGCTATACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGCG CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCTAT
501 CATCATCGTC GGACTGCTGA TGGCATATAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGTTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC
651 CCATCTTGCC ATCCAATTCC ACAAAATGGT GGAATACTC GAAAACTCG
701 TTGCCAAGAG ACGCAACCTG CTCCATCACG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAAGT ACCCGCATGG
851 ATACGCTGGC CGGGGAATG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 TTGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AACGGACAA ACGGTTACCC
1001 TGCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCTT TGCCAACGAA
```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLRFORIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLRFORIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
g585	MKLRFORIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGDEKDDILNRYIDNYTIERARLFAANNPHSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEEYLFPIKWDNHAQRLSPFLIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILGNGMDRVAERELEDRCQQVRDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTSLRLETNS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTTGC CGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTGCAC GACCGCGACG ACGAATTGTC

```

```
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGCC CCGCGGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTACCCG TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCAGACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```
a585.pep
1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGEKKD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKEHRL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQOE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMO
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*
```

m585/a585 99.8% identity in 468 aa overlap

```

      10      20      30      40      50      60
m585.pep MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
|||||
a585      MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
      10      20      30      40      50      60

      70      80      90      100     110     120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGEKKDILNRYIDSYTIERARLFAAGHPHNSLVHIE
|||||
a585      DAGAREILTEWKDSPVSSGVYVIQGEKKDILHRYIDSYTIERARLFAAGHPHNSLVHIE
      70      80      90      100     110     120

      130     140     150     160     170     180
m585.pep YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
|||||
a585      YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
      130     140     150     160     170     180

      190     200     210     220     230     240
m585.pep NIAKPIRILGNMMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL
|||||
a585      NIAKPIRILGNMMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL
      190     200     210     220     230     240

      250     260     270     280     290     300
m585.pep LHHVSHEMRSPLARMQAIVGLIQAQPKQOEQYLKRLEGELTRMDTLAGELLTSLRLETNS
|||||
a585      LHHVSHEMRSPLARMQAIVGLIQAQPKQOEQYLKRLEGELTRMDTLAGELLTSLRLETNS
      250     260     270     280     290     300

      310     320     330     340     350     360
m585.pep MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV
|||||
a585      MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV
```

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTNNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTNNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccaaa accgtgctgc ttcccaaat
151 caggaagcgg cggcgggtgt ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcgtta cgatgttgcc gaaggctcatt tgaatatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401 tggcggtgtg gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAEISKL QQSYPHSISA AQATLMMAAT
101 EFDAQRYDVA EGHKQWVLSN QKDSLIALA AQLRGVLLQ QKKYDAALAA
151 LDFPVEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAACT TTAAATATTT
51  TTGGAAGAAC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT ACCCAAACCT CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAAAAAAT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCTG TCGCGAATTG
601 GTTCAATGA AACTTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51  QEAAAVLANI VEKAQSKAPQ SEINAEITKL QQSYPHSISA AQATLMMAAT
101 EFDAQRYDVA EGHKQWVLSN QKDSLIALA AQLRGVLLQ QKKYDAALAA
151 LDFPVEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTTGKWL <u>FALLI</u> LAALGYLGYTVYQNRKVSQNQEAAAVLANI					

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAAALGYLGYTVYQNRAASQNEAAAVLANI
           10      20      30      40      50      60
m586.pep  70      80      90      100     110     120
           VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQWVLSN
           70      80      90      100     110     120
m586.pep  130     140     150     160     170     180
           QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180
m586.pep  190     200     210
           LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATGTGCAAC CAAAAAGACA GCCTGATCCA GGCCTTGCGC GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCTG TCGCGAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51 QEAAAVLANI VEKAQNKAPQ SEINAELAKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLQWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

m586.pep  10      20      30      40      50      60
           MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQN
           10      20      30      40      50      60
m586.pep  70      80      90      100     110     120
           VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKQWVLSN
           70      80      90      100     110     120
m586.pep  130     140     150     160     170     180
           QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
a586	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgccc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101  aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151  gccgcacttg ccgcaccggg ttacattcaa accggcgcaa cctcgtttat
201  ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251  ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301  ggcagcggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351  caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401  ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaaagc
451  acggttttac aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501  gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151  TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101  AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151  GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201  CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251  TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301  GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351  CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401  CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451  ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501  CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551  CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601  TACAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGCTG
651  CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701  CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751  GCCCATTTTC GCGCAGGTTT CGGTTTACC AAAACCACGG CTTTAAACGC
801  ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTG
851  GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151  TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201  YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251  AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

```
a587.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAAGGTC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCTC CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCGGA AACAAACGGA TGTCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACAAA
601 TACAAAGCAG CGAATTACTG GATGCTGAAT CCAATATAT CCTTCGCGCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCAACG CTTTAAACGC
801 ATCCGACGTG TTCAACGGTT CAGGGCAAA GAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

a587.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNRR
51	AELAAPVYIQ	TGATSFIIPI	TEIQENGST	DMLVGTGLRL	YGLTGNTDIY
101	GSGSYLWHEE	RKLDGNGKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLSSNTK
201	YKAGNYWMLN	PNISFANDR	ISLTGGIOWL	GKQPDRLDGK	KESARNTSTY
251	AHFGAGFGFT	KTTALNASAR	FNVSGQSSE	LKFGVQHTF*	

```

      10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNR AELAAPVYIQ
          |||||:|||||||||||||||||||||||||||||||||||||
a587      MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNR AELAAPVYIQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m587.pep  TGATSFIPIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSGSYLWHEERKLDGNSKTR
          |||||:|||||||||||||||||||||||||||||||||||
a587      TGATSFIPIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```


	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1   atgcttaaac atctcgcat cctactgccc gccatgatgt tgcgcctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgccaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRNYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCC TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPHKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGPAGKGTWRCQDGRNYTGS
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g588           MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
g588           FKNGKFDGQGVYTVAAAGREVLFEPNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
g588           YYEMRTRHDX
               130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGCGCA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

               10      20      30      40      50      60
m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGPAGKGTWRCQDGRNYTGS
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a588           MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGDKGPKAGKGTWRCQDGRNYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a588           FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
               |||||
a588           IMKCENGMIKEVKLPKNKX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tggtgaacaa aaaagatttt gtcgaatcgg
101 cgggagttaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgtcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg ggcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tgggtatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgacca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcggaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaaatc aatcccgaag
851 agaaaaaggc gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggc
901 acgctgggtg accgcgcgcg gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggctg attaaggcgg attggacggg
1101 cgcactgatg cacgcctgtg ccgttttggg gattgcctgc ccgtgcgcg
1151 tcggctctggc gacccttggc gcgattatgg tcggcatggg caaagcgggt
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagcca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc gcgcgtttat tacgttccc acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgcgt
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccc
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcaacttc cgacgcgttg
1651 aaagccgata ccgcccgaag cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 acaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaacccg tggcgatggg
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcgggtgc gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcggtt tcgggtattgg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPI YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSWG ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAI PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRFPQVAAY YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTGCCGAGC GAAGAGGCGC AGGTAGTGTG TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTT

```

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CCGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCCTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AAGCCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGC GCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTGCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CCGTATTGCG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCCGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCA
1451 AAACCGTTGT CCGCGCAGGC ATTACCGCG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TGCGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CCGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CCGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCCTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCC
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTTC
2051 CTCTCGCCGC GCTTGGCTTT TAAATCCCG TCATCGCTGG CGCGGCAATG
2101 CGCGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLFTINVFPFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLKLTP TQVNVQRNGE WKQLPIDVQV IGDILIRANHG
251 ERIAADGIIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVEVP AVVGIALLTFF
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEAA AHVDAVVLDAK TGTLTGEGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10          20          30          40          50          60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTTSVADIANKI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
	:					
g589	EIPAAQNAQTVVGAGITAEEVGVGLVKSGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAGG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCCCTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGCGCA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCGTATATCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAAAC CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCAATC ACGGCGAAGC CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCAGAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGCGCG GCGCGTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCCA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCG TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATCGC TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

```

```
a589.pap
1  MQQKVRFAQIE  GMTCCACASR  IEKVLNKKDF  VESAGVNFAS  EEAQVVFDD
51  KTSVADIARI  IEKTRGYGAK  KTEDTLPQPE  AEHHIGWRLW  LLLAINIPFL
101 IGMVGMMLKG  LNWTRGDWML  SPLLQFALAS  VVQLWLAVPF  YKSASAWIKG
151 GLANMDVLVT  IGTVSIYLYS  VYMLFFSPHA  AYGMAHVYFE  VGMIVIGFVS
201 LGKFLEHRTK  KSSLNSLGLL  LKLTPTQVNV  QRDGEWRQLP  IDQVQIGDLI
251 RANHGERIAA  DGIIESGSGW  ADESHLTGES  NPEKKKAGGK  VLAGALMTEG
301 SVVYRAAQLG  SQTLLGDMMN  ALSEAQGSKA  PIARVADKAA  AVEVPAVVGI
351 ALLTFIATWL  IKGDWTLALM  HAVAVLVIAI  PCALGLATPA  AIMVGMGKAV
401 KHGIWFKDAA  AMEEAAHVDA  VVLDKTGTLT  EGKQPVAAVY  CVPDGSDDED
451 ALYRIAAAVE  QNAAHPLARA  IVSAAQARGL  EIPTAQNAQT  TVGAGITAEV
501 KGAGLVKAGK  AEFAELTLPK  FSDGVWEIAS  VVAVSVNGKP  IGAFALADAL
551 KADTAEAIGR  LKKHNIDVYI  MSGDNQGTVE  YVAKQLGIAH  AFGNMSPRDK
601 AAEVQKLKAA  GKTVAVMVGD  INDAQNLAAA  NVSFAMKGGG  DVAEHTASAT
651 LMQHSVNQLA  DALSVSRATL  KNIAQNLFFA  FFYNILGIPL  AALGFLNPVI
701 AGAAMAASSV  SVLSNALRLK  RVKID*
```

		10	20	30	40	50	60
m589.pep		MQQKIRFQIEG	MTCQACASRIE	KVLNKKDFVES	SAGVNFASEEA	QVVFDDSKTSV	ADI
		:					
a589		MQQKVRFFQIE	GMTCCQACASRIE	KVLNKKDFVES	SAGVNFASEEA	QVVFDDSKTSV	ADI
		10	20	30	40	50	60
		70	80	90	100	110	
m589.pep		IEKTGYGAKEK	TEDTLPQPEAE	HHIGWRLWLL	FTINVPFLIGM	AGMMIG----	RHDWMI
a589		IEKTGYGAKEK	TEDTLPQPEAE	HHIGWRLWLL	LAINIPFLIGM	VGMMMLKGLN	WNRHDWML
		70	80	90	100	110	120
		120	130	140	150	160	170
m589.pep		PPLWQFALASV	VQLWLAI	PFYKSAWASIK	GGLANMDVL	VTIGTVSIYLY	SVYMLFFSPHA
			:				
a589		SPLLQFALASV	VQLWLAV	PFYKSAWASIK	GGLANMDVL	VTIGTVSIYLY	SVYMLFFSPHA
		130	140	150	160	170	180
		180	190	200	210	220	230
m589.pep		AYGMAHVYFEV	GMVIGFVSLG	KFLEHRTKKS	SLNSLGLLLK	LTPQTQVNVQ	RNGEWKQLP
a589		AYGMAHVYFEV	GMVIGFVSLG	KFLEHRTKKS	SLNSLGLLLK	LTPQTQVNVQ	RDGEWRQLP
		190	200	210	220	230	240

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	250	260	270	280	290	300
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFTIVTWL					
a589	310	320	330	340	350	360
	SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFTIVTWL					
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	370	380	390	400	410	420
	IKGDWTLALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
a589	430	440	450	460	470	480
	VVLDKTGTLTGEGKQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	490	500	510	520	530	540
	EIPTAQNQITIVGAGITAEVKGAGLVKAGKAFAELTLPKFSDGVWEIASVAVSVNGKP					
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAIIGRLKKNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	550	560	570	580	590	600
	IGAFALADALKADTAEAIIGRLKKNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
a589	610	620	630	640	650	660
	AAEVQKLKAAGKTVMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
a589	670	680	690	700	710	720
	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgctgca gtattgctcg gcggttgcctt
51  ggggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccagc
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaaac ctttttggg aaacaagtc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```



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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcy cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaaatac ggcccgtg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgccc cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaataattg
1151 atgtgggccc aaaaatcatg tttaaaggca tgaagaagga agatttgaa
1201 cagtggggac tgatgtttaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgctt gatggtggac agtacgggtc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:
g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGKAEES LTQOOKILOK TGFLTVESHO
51 YDRGWFTSTE TTVIRLKPDL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSUNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGATATA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCCGAG TTCAAATACG CGCCTGAAAC
201 GGAATAAGTT CTGGAACGCT TTTTGGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAAGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCCG TATTGGACAT
951 TAAACTTTTC CGATTACGC TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGCGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep..(partial)

```
1  ..WFTSMETTVI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE PKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSV
101 AFDYEEELSGI XLHWEXLTGE TVYQKGFKSY RNGYDAPLFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT EQRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPOKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT L NGDQIDTAIS LKNNQLKLNG KTLQNEPEPD
451 FDEGGMVSEP QQ*
```

m590 / g590 93.1% identity in 462 aa overlap

```
m590.pep                                10      20      30
                                WFTSMETTIVIRLKPELLNNARKYLPDNLKT
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
VKAESLSTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPELLHNAQKYLPDNLKI
      30      40      50      60      70      80

m590.pep                                40      50      60      70      80      90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
      90     100     110     120     130     140

m590.pep                                100     110     120     130     140     150
GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLFKIKLADKGDAA
      150     160     170     180     190     200

m590.pep                                160     170     180     190     200     210
FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
      210     220     230     240     250     260

m590.pep                                220     230     240     250     260     270
PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
      270     280     290     300     310     320

m590.pep                                280     290     300     310     320     330
SALTVLKRKFAQISAKKMTTEEQRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SALTVLKRKFAQISAKKMTTEEQRNDLIAAVKGDASGLFTHDPVLNLIKIFRFTLPQKID
      330     340     350     360     370     380

m590.pep                                340     350     360     370     380     390
VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPOKMLEDLAVSQAGNIFSVNAEDEAEG
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPOKMLEDLAVSQAGNIFSVNAEDEAEA
      390     400     410     420     430     440

m590.pep                                400     410     420     430     440     450
RASLDDINETLRLMVDSTVQSMAREKYLTLDGNDQIDTAISLKNQKLNGKTLQNEPEPD
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RASLADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNQKLNGKTLQNEPDPD
      450     460     470     480     490     500

m590.pep                                460
FDEGGMVS-EPQQX
g590                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
FDEGDMVSGQPHX
      510
```

```

a590 .seq
1 ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51 GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA CGGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG CGTGGTTTAC CTCTACGGAA ACAGCGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACCG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTGTGAAAA AGTGCAATTTC GATTCCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA CCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAANAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACC GTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATACTT TCCGATTACG GATTGCCATG GGAATAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAA ATGCTGGAAG ACTTGCGGTT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG CGAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGC GCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```

a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEEs LTQQQKILQE AGFLTvesHQ
51  YERGwETSTE TTVIRLKPEL LHNAQKYLPD NLKTVLEQPV TLVNhITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSPAFDYEE LSGIRLHWEG LTGETVYQKL FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LAGTSSNLTG EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGGFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETRLRMVD STVQSMAREK YLTlNGDQID TAISLkNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPOO*

```

m590/a590 97.8% identity in 462 aa overlap

```

                                10      20      30
m590.pep                      WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a590      VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTIVIRLKPPELLHNAQKYLPDNLKT
              30      40      50      60      70      80

              40      50      60      70      80      90
m590.pep      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a590      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
              90      100     110     120     130     140

              100     110     120     130     140     150
m590.pep      GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLEFKIKLADKGDAA

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|||||
a590 GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
150 160 170 180 190 200

160 170 180 190 200 210
m590.pep FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
|||||
a590 FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
210 220 230 240 250 260

220 230 240 250 260 270
m590.pep PNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGOFRFDTLVYGDEKYGPLDIHIAAEHLDA
|||||:|||||
a590 PNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGOFRFDTLVYGDEKYGPLDIHIAAEHLDA
270 280 290 300 310 320

280 290 300 310 320 330
m590.pep SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
|||||:|||||:|||||
a590 SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
330 340 350 360 370 380

340 350 360 370 380 390
m590.pep VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
|||||
a590 VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
390 400 410 420 430 440

400 410 420 430 440 450
m590.pep RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKTLQNEPEPD
|||||
a590 RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKTLQNEPEPD
450 460 470 480 490 500

460
m590.pep FDEGGMVSEPQOX
|||||
a590 FDEGGMVSEPQOX
510

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

1 ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51 GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCTGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CGGCCTTCGA TTATGAAGAG CTGTCCGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TCAAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCAATTC GATTCCGAAA CTTCAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGA AAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGAAGTGTCA CCAACAATCC
1101 CGTATTGGAC ATTA AAACCT TCCGATTAC GCTGCCATCG GGA AAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

```
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```
1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE TGFLTVESHQ
51 YERGWFSTME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTOAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT LKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNLNGDQID TAISLKNQNL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590-1/g590 93.6% identity in 516 aa overlap

m590-1.pep	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFSTME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTE					
	10	20	30	40	50	60
m590-1.pep	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTOAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLPDNLKIVLEQPVTLVNHITHGPFAGGFGTOAHIEEFKYAPE					
	70	80	90	100	110	120
m590-1.pep	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
m590-1.pep	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
m590-1.pep	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFASTKTGESGAFINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFASTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
m590-1.pep	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKMTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKMTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
m590-1.pep	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDPVLNIKIFRFTLPQGKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
m590-1.pep	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQID					
g590	MLEDLAVSQAAGNIFSVNAEDEAEARASIAADINETLRLMVDSTVQSMAREKYLTLDGNQID					
	430	440	450	460	470	480
m590-1.pep	490	500	510			
m590-1.pep	TAISLKNQNLKNGKTLQNEPEPDFDEGGMVS-EPQQX					

g591.seq

```
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTGATACG CGCGAAGCGC AAGTATCAGA AGCCATATTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCTCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTTGCTG TACGGACTGa gctTtctctt
351 cggcgtaaCC GAACTGCGGC CCTatgtcgg cacagtcgaA cccgacacc
```

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1  LQTLAIFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCGCGC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCC CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTC AAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51 DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIAARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYPSPVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMAVAFFND VTRLLG*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
g591	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTV	EPDTIAARAG	FQSGDKIQSV	NGTPVADWGS	AQTEIVLNLE	AGKVAVGVQTA
g591	ELRPYVGTV	EPDTVAARTG	FQSGDKIQSV	NGVSVQDWSS	AQTEIVLNLE	AGKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTI	DAAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVEKGSPEAK	AGLKPGRDLTA
g591	SGAQTVRTI	DAAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVEKGSPEAK	AGLKPGRDLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASW	QEWANLTRQS	PGKKITLNYE	RAGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASW	QEWANLTRQS	PGKKITLTYE	RAGQHTADIR	PDTVEQPDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQI	RRSYRPSVVR	AFGMGWEKTV	SHSWTTLKFF	GKLISGNASV	SHISGPLTIAD
g591	PDRAWDAQI	RRSYRPSVVR	AFGMGWEKTV	SHSWTTLKFF	GKLISGNASV	SHISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLLP	VVPVLDGGHL	LVFYTAEWIR	GKPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLLP	VVPVLDGGHL	LVFYTVEWIR	GKPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFGALMM	LMMAVAFFND	VTRLLGX			
g591	GLRFGALMM	LMAAAFFND	VTRLLGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:
a591.seq


```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCTCG CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTCGACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGCGCT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT GGCACCTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAACATC GGTTTGCGCT TCGGCGTTGC CCTCATGATG CTGATGATG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

a591.pep

```

1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGL PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNL L PVPVLDGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMVAFFND VTRLIC*

```

m591/a591 99.6% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG DTEWCLAPIP					
a591	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG DTEWCLAPIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m591.pep	LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT					
a591	LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m591.pep	ELRPYVGTVE PDTIAARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQTA					
a591	ELRPYVGTVE PDTIAARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDA AAGTPEAGKIA KNQGYIGL MPFKITTVAGG VEKGSPEAKA GLKPGDRLTA					
a591	SGAQTVRTIDA AAGTPEAGKIA KNQGYIGL MPFKITTVAGG VEKGSPEAKA GLKPGDRLTA					
	190	200	210	220	230	240

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSIISLGVNLNLLPVPVLDGGHLLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSIISLGVNLNLLPVPVLDGGHLLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg  acgtgttcgg  tcagattttt  tcgggcgcg  tcaaattcga
51  cgcggcagca  ggcggcctac  tcggcggtct  gatttcgcaa  acgatgatga
101 tgggcatcaa  acgcggcctg  tattccaacg  aggcgggtat  gggttccgcg
151 ccgaacgccc  ccgcgcgcgc  cgaagtgaag  caccctgttt  cgcaaggtat
201 gattcaaatg  ctgggcggtg  ttgtcgatac  catcatcggt  tgttcttgca
251 ccgccttcat  catcttgatt  taccaacagc  cttatggcga  tttgagcggt
301 gcggcgctga  cgcaggcggc  gattgtcagc  caagtggggc  aatggggcgc
351 ggggtttcct  gccgtcatcc  tgtttatggt  tgccttttcc  accgttatcg
401 gcaactatgc  ctatgccgag  tccaacgtcc  aattcatcaa  aagccattgg
451 ctgattaccg  ccgttttccg  tatgctgggt  ttggcggtgg  tctatttcgg
501 cgcggttgcc  aatgtgcctt  tggctctgga  tatggcggat  atggcgatgg
551 gcatcatggt  gtggatcaac  ctgctcgcca  tctgtctgct  ctgcgccattg
601 gcgtttatgc  tgcgtcgcca  ttacacgcgc  aagctgaaaa  tgggcaaaaga
651 ccccgagttc  aaactttccg  aacatccggg  cctgaaacgc  cgcatacaat
701 ccgatgtttg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF  SGAFKFDAAA  GLLGLGISQ  TMMGIKRL  YSNEAGMGSA
51  PNAAAAAEVK  HPVSQGMQM  LGVFVDIIV  CSCTAFILI  YQQPYGDLG
101 AALTQAAIVS  QVGWAGAGFL  AVILFMFAFS  TVIGNYAYAE  SNVQFIKSHW
151 LITAVFRMLV  LAWVYFGAVA  NVPLVDMAD  MAMGIMAWIN  LVAILLLSPL
201 AFMLLRDYTA  KLKMGKDPEF  KLSEHPGLKR  RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG  ACGTGTTCGG  TCAGATTTTT  TCGGGCGCGT  TCAAATTCGA
51  CGCGGCAGCA  GGCggcctac  TCGGCGGTCT  GATTTCGCAA  ACGATGATGA
101 TGGGCATCAA  ACGCGGCCTG  TATTCCAACG  AGGCGGGTAT  GGGTTCGCGG
151 CCGAACGCCG  CCGCGGCCGC  CGAAGTGAAA  CACCCTGTTT  CGCAAGGTAT
201 GATTCAAATG  CTGGGCGTGT  TTGTCGATAC  CATCATCGTT  TGTCTTGCA
251 CCGCCTTCAT  CATCTTGATT  TACCAACAGC  CTTACGGCGA  TTTGAGCGGT
301 CGCGCGCTGA  CGCAGGCGGC  GATTGTCAGC  CAAGTGGGGC  AATGGGGCGC
351 GGGCTTCCTC  GCCGTCATCC  TGTATTGTT  TGCCTTTTCC  ACCGTTATCG
401 GCAACTATGC  CTATGCCGAG  TCCAACGTCC  AATCATCAA  AAGCCATTGG
451 CTGATTACCG  CCGTTTCCG  TATGCTGGTT  TTGGCGTGGG  TCTATTTCCG
501 CGCGGTTGCC  AATGTGCCTT  TGGTCTGGGA  TATGGCGGAT  ATGGCGATGG
551 GCATTATGGC  GTGATCAAC  CTTGTCGCCA  TCCTGCTGCT  CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

m592.pep	10	20	30	40	50	60
	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRG LYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRG LYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
m592.pep	70	80	90	100	110	120
	HPVSQGM IQM LGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVS QVGQWGAGFL					
g592	HPVSQGM IQM LGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVS QVGQWGAGFL					
	70	80	90	100	110	120
m592.pep	130	140	150	160	170	180
	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
m592.pep	190	200	210	220	230	
	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCCG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGCGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggctcg
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcgggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtcgggcccgc acggcgggcga aattcggtcg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctcgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacgggtg gcaactggcg gcgctttggt tgcgcgcctc
451 tccctgctgt tgctggatga atcgttttcc agtttgaca cgcatttgca
501 cgaccggctg cgccgtatga ccgcgaacg catccgcaag gccggcgac
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac gccggcgac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgca gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtgca ggctgcgccg ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaatgca cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctgctccggg ctttccggcg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacgcta tttccggaac cggtagcggtc
901 cgcattccgg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAE LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTEAIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSL RLSAVHPEHGE LTLNLTVGQH TDGISNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTGCGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGAGAAA ACATTACCCG

```

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGGC CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTTGGACGA ATCGTTTTTC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCCG CTGATGGGTT
701 TGCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLENLGLCKR FGNTKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
  51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

```

              10      20      30      40      50      60
m593.pep      MLENLGLCKRFGNTKTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIIVRPDGGGEIWL
              |||||  ||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           MLENLGLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIIVRPDGGGEIRL
              10      20      30      40      50      60

              70      80      90     100     110     120
m593.pep      NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEAEERLAMAALAEVG
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG
              70      80      90     100     110     120

              130     140     150     160     170     180
m593.pep      LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK
              130     140     150     160     170     180

              190     200     210     220     230     240
m593.pep      GGIPAVLVTHSPEEACTTADEIIVMHKGRI LQYGTPELTVKTPSCVQVARLMGLPNTDDN
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g593           GGIPAVLVTHSPEEACTTADEIIVMHGEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD
              190     200     210     220     230     240

```

938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	::: :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGA CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGGGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACC GAGCCTGAN AAACTTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCGCCCTC
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCATCC
551 CTGCCGTTT GTTAACGCAT TCGCCGAAG AGGCCTGCAC GCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCGA
651 AACCTTGTT CAAACGCCTG CCGGCGTGCA GGTGCCCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPKX KLSGGGKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMCECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	: : : : : : : : : : : : : : :					
a593	MLELNLCKRFGGKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAEERLAMAALAEVG					
	: : : : : : : : : : : : : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGGKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	: : : : : : : : : : : : : : :					
a593	LENEHRKPKXKLSGGGKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLPNTDDN					

a593		: : : :
	GGIPAVLVTHSPPEEACTAADEIAVMHEGKILQCGTPETLVTQTFAGVQVAHLMGLPNTDDD	: :
	190 200 210 220 230 240	
m593.pep		250 260 270 280 290 300
	RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPHGILWLNLDMRHAGAVSGKDTR	:
a593		: : : :
	RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPHGILWLNLDMPHAGEISGNDR	: :
	250 260 270 280 290 300	
m593.pep		310
	IHIEREIVFRFX	
a593		: :
	IHIEDREIVFRFX	
	310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

g594.seq..

1	atgggtgcag	ataccgatgg	cgacaaggat	gttcggctta	atcgaacggg
51	tctcgtttt	agcatactcc	ggctgctgtt	ccgcatcgga	attgggatcg
101	gtaagttcgc	cgttcaggcc	tttcagggtt	ttaagctggt	gatctgtacg
151	gttgagcacc	caaatcggtt	tgccttgcca	ctcggcggtc	agcagctgac
201	ccgcttcgat	tttactgaca	tccacctcga	cggcagcacc	ggaggccttg
251	gctttttccg	aagggaaaaa	actggccaca	aacggcggtg	ccacacccaa
301	tgctgccact	ccgcccgcgc	cgcaggtcgc	aagtgtcagg	aaacggcggc
351	ggccggtgtt	gattttctta	ttattccaata	ttcagtcgtc	ctaataatatt
401	gggaatgcg	agccattaaa	cattgcaatt	ttaccagatt	tgcagtgata
451	ctcaaagcat	tatttaaaat	aaggtaa		

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pep

1	MGADTDGDKD	<u>VRLNRTGLVF</u>	<u>SILRLLF</u> FRIG	IGIGKFAVQA	FQVFKLLICT
51	VEHPNREALP	LGGQQLTRFD	FTDIHLDGST	GGLGFFRREK	TGHKRRCHTQ
101	CCHSARAAGR	KCQETAAAVV	<u>DFLIHYSV</u> V	<u>LIFWECRAIK</u>	HCNFTQFAVI
151	LKALFKIR*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

1	ATGGGTGCAG	ATACCGATGG	CGACAAGGAT	GTTCCGGCTTA	ATCGAACGGG
51	TCTCGTTTTT	AGCATACTCC	GGCTGCTGTT	CCGCATCGGA	ATTGGGATCG
101	GTAAGTTCGC	CGTTCAGGCC	TTTCAGGTTT	TTAAGCTGCT	GATCTGTACG
151	GTTGAGCACC	CAATCGGTC	TGCCTTGCCA	CTCGGCGGTC	AGCAGCTGAC
201	CCGCTTCGAT	TTTACTGACA	TCCACCTCGA	CGCAGCACC	GGCGCCTTG
251	GCTTTTTCCG	AAGGGAAAAA	ACTGGCCACA	AACGGCGTTG	CCACACCCAA
301	TGCTGCCACT	CCGCCC GC GC	CGCAGGTCGC	GAGTGT CAGG	AAACGGCGGC
351	GGCCGTTGTT	GATTCTTTGA	TTATCCATTA	TTCAGTCGTC	CTAATATTTT
401	GGGAATACCG	AGCCATAAA	CGTTGCAATT	TTACCCAGTT	TGCAGTGATA
451	CTCAAAGCAT	TATTTAAAT	AAGGTAA		

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

m594.pep

1	MGADTDGDKD	<u>VRLNRTGLVF</u>	<u>SILRLLF</u>	<u>FRIG</u>	IGIGKFAVQA	FQVFKLLICT
51	VEHPNRFALP	LGGQQLTRFD	FTDIHLDGST	GGLGFFRREK	TGHKRRCHTQ	
101	CCHSARAAGR	ECQETAAAVV	<u>DFLIHYSV</u>	<u>LIFWEYRAIK</u>	RCNFTQFAVI	
151	LKALEKIR*					

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTCAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
51  gaccgcgtgc cagccgcccg agcgaggaaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

```



```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgga aaactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacccaaa
```

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLTVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPIV DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRIGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGTGAAA AACTGTCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTTGC
 801 GTTCTCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGCGGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQAVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLTVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRIGILGLK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSIQAVNDNACEPMELT					
g595	MRKFNLALSVMALGLTACQPPEAEKAAPASGETQSANEGGSVGIQAVNDNACEPMNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m595.pep      VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
                |||||||:|||||
g595           VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRLLPGEYEMTCGLLT
                70      80      90      100     110     120

                130      140      150      160      170      180
m595.pep      NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
                |||||||:|||||
g595           NPRGKLVVAD SGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
                130      140      150      160      170      180

                190      200      210      220      230      240
m595.pep      KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGA KDAGFTGFHRIEYALWVEK
                |||||||:|||||
g595           KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGA KDAGFTGFHRIEHALWVEK
                190      200      210      220      230      240

                250      260      270      280      290      300
m595.pep      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEVAGSKISGEEDRYSHTD
                |||||||:|||||
g595           DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVG GASELIEEAAGSKISGEEDRYSHTD
                250      260      270      280      290      300

                310      320      330      340      350      360
m595.pep      LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FETYDKLG
                |||||||:|||||
g595           LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FETYDKLS
                310      320      330      340      350      360

                370      380      389
m595.pep      EADRKALQASINALAEDLAQLRGILGLKX
                |||||||:|||||
g595           EADRKALQAPINALAEDLAQLRGILGLKX
                370      380

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1   ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCA GTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAC TGACC GTGCCAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACGCG CACGAAGCGG GATTTGAAA AACTGTCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGCGGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCGGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAC TGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGA ACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTT AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCTT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1   MRKFNL TALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
51  DNACEPMELT VPSGQVV FNI KNNSGRKLEW EILKGMVVD ERENIA PGLS

```

```

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

```

              10      20      30      40      50      60
m595.pep      MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a595           MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
              10      20      30      40      50      60

              70      80      90     100     110     120
m595.pep      VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a595           VPSGQVVFNKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
              70      80      90     100     110     120

              130     140     150     160     170     180
m595.pep      NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a595           NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
              130     140     150     160     170     180

              190     200     210     220     230     240
m595.pep      KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a595           KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
              190     200     210     220     230     240

              250     260     270     280     290     300
m595.pep      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a595           DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
              250     260     270     280     290     300

              310     320     330     340     350     360
m595.pep      LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG
              |||||||||||||||||||:||||||||||||||||||||||||||||||||||
a595           LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG
              310     320     330     340     350     360

              370     380     389
m595.pep      EADRKALQASINALAEDLAQLRGILGLKX
              |||||||||||||||||||
a595           EADRKALQASINALAEDLAQLRGILGLKX
              370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgctg aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101  cgacagaccg ctacttcttc gacaacgccg ccgaatggat tttggaactc
151  gaccgctggc acggcattcc gtggaaaggc aattactcgt cttggctgga
201  gcagaaagaa aaacgcttgg aaaacgaggg gaaatccgaa gccgcgcgcg
251  tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301  cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351  ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401  ccgagcgttt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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451   ttcggcgata aagtgcctgat tgacggtttg agcttcaaag tgcggcgagg
501   cgcgattgtc ggcacatcatc gcccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagccgcy aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccggc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcgccggt ctgcacttgg caaaaacctt gttggcgggc ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcy
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcaccaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLENEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYEY QKRNETQEIF IPVAERLGNE VIEFVNVSXS
151 FGDKVLIDGL SFKVPAGAIIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQYEYA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTT TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCGCGG TTGCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TGCGGAATCG
601 TCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTGGAAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGCCGCCCA AGCCAAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTGA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GTTCAGTTTG AAATTTCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCCTG
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCTT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

```

1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AOKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

m596.pep      160      170      180      190      200      210
               LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLD EPTNHLDAESVEWLEQFLVRFP
g596          100      110      120      130      140      150
               MLLLD EPTNHLDAESVEWLEQFLVRFP
               10      20      30

m596.pep      220      230      240      250      260      270
               VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQ
g596          40      50      60      70      80      90
               VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQ

m596.pep      280      290      300      310      320      330
               LEWVRQNAKGRQAKSKARLARFEEMS NYEYQKRNETQEIFIPVAERLGNIEVIEFV
g596          100      110      120      130      140      150
               LEWVRQNAKGRQAKPKARLARFEEMS NYEYQKRNETQEIFIPVAERLGNIEVIEFV

m596.pep      340      350      360      370      380      390
               FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDGGEVKIGQTVKMSLID
g596          160      170      180      190      200      210
               FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID

m596.pep      400      410      420      430      440      450
               QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
g596          220      230      240      250      260      270
               QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR

```

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLLDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330
	520	530	540	550	559	
m596.pep	ACEGDSKWVFFDGNVQEYEADKKRRLGEEGAKPKRIKYKPVTRX					
	:					
g596	ACEGDSKWVFFDGNVQEYEADKKRRLGEEGAKPKRIKYKPVTRX					
	340	350	360	370		

```
a596.seq
1 ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTGTGTGCC
51 GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTTCTTTC TTCCCCGGCG
101 CGAAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGTCTG
151 CGGATTATGG CGGGCGTGGG TAAAGAATTT GAGGGCGAAG CGGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG CGGTTTGGAA GCGATTATTG
401 CGGCGGGTTC GCTCACGGGC GCGGTGCGG AACACGAATT GGAATTCGCT
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTCT
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TCGGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGGCG TCCCCCGGTA CAGTCGTTTG
651 CGTAAACACAC GACCGCTACT TCCTCGACAA CGCCCGCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA TCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGGAAAAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAACTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGC GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGACGTTGA TTGACCAAAG CCGCGAAGT
1201 TTGCAAAACG ACAAAAACCG GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCGCG CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GGCAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTCG
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGTTCTCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGCGCAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC CGGTTAA
```

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a596.pep
1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVSTG VESGLGEVAA
101 AQKRLEEYVA EYANPDAFD ALAAEQGRLE AIIATGSSRE GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQEKRLN EAKSEAAVRK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNVIEFV NVSKFSQDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPD SGEVKIGQTVK MSLIDQSRG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKKRR LGEEGTPKPR
551 IKYKPVTR*

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BNSDOCID: <WO 9957280A2 | >

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNIEVFNVSFSFGDKVLIDDLSEFKVPAGAIVGII GP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEVFNVSFSFGDKVLIDDLSEFKVPAGAIVGII GP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFFKMISGKEQPDSEGVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFFKMIAGKEQPDSEGVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLLDPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```



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151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGGCGGAA CAGACGGAAG GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAaagcc
601 gaacaccgCA TTcaggAtgc ggaagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGA AAGCGGTGTT CTATTCCTACT
901 GCGCCTGCAG CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACG AGCGGGTTCG TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTGAG GTGTTGAACC
1151 CTTGCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFOK
51 LNTELNRLLK EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QKALAVQEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQV VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAAGC CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGC CGAGGCTTGG GACAAAGTCC AAAAACTCAA TACCGAGCTG
151 AACCCTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGAAGAACCG CGAACC GGCTTTCGCT CAGAAAAACC GCTTTTTCG
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAAACGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAA CAACAATGAG CTGCCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAACTGTC TGGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCATAT TTGGAAGGCG GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAAGT GTCGTGGTGC ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNVA ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQKAL AVQEQKINNE LARLKKIQAN VQSLLKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLNSNL EKKKAEHRIQ
201 DAEAKRKLA ERLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDNRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDDGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGVLNPS SWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKLQEEIRIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKLQEEIRIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QOKALAVQEQKINNELLARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QOKALAVQEQKINNELLARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSGWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTCAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAAAACG	GAAGTCGCCG	CTACGAAAGC
201	GCAGATTTC	CGTTTCGTAT	CGGGGAAC	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCCCTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCTCC	AATCGGGAAG	TTGTCAAGGA
351	TTTGGAAGAA	CAGCAGAAAG	CTTGGCGGT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CCGTTTGAAG	AAAATTCAGG	CAAACGTGCA	ATCCCTGCTG
451	AAAAAACAGG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	CCGCAGACA
501	GAATGCCAAA	ATGCCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTGGAGAA	GAAAAAGGCC
601	GAACACCGCA	TTCAGGATGC	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAGA	AGCGGCGCAG	CAGAAGGCTG
701	AAGCACGACG	TGCGGAAATG	TCCAACCTGA	CCGCCGAAGA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACGT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GGCAGAACCG	GAGCGGCGGC	GATGTTTGGG	AAGGCGTGTT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

```
951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```
1 MLLHVSNSLK QLQEERIQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPSWIR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

```

          10      20      30      40      50      60
a597.pep  MLLHVSNSLKQLQEERIQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT
          |||
m597      MLLHVSNSLKQLQEERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT
          10      20      30      40      50

          70      80      90     100     110     120
a597.pep  EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          |||
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90     100     110

          130     140     150     160     170     180
a597.pep  QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          |||
m597      QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

          190     200     210     220     230     240
a597.pep  QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          |||
m597      QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

          250     260     270     280     290     300
a597.pep  SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST
          |||
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

          310     320     330     340     350     360
a597.pep  APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS
          |||
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

          370     380     390
a597.pep  SGSLPDGEEGLYLQIRYQGQVLNPSWIRX
          |||
m597      SGSLPDGEEGLYLQIRYQGQVLNPSWIRX
          360     370     380
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

g601.seq

```

1   ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCTATGAT GGGCATCGCC TCGGTGCGCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCGCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcgggtca
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttccccgat
601 gattGTTTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

g601.pep

```

1   MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTAA KAVMSRSARV IMESWVRVPD
201 DCF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

m601.seq

```

1   ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CCGCTTTGGA AAAATTTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACAGGTTG
601 CCTGAGGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

m601.pep

```

1   MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDQGWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					
	70	80	90	100	110	120

```
a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCGACAC GTTTTCCTGA
101 ATGCCGCGCA TTGGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACGCGCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGTCTTG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCATGATG GATTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCGCGAGGC
451 GGCGAACGCG GTAAAGAAAG GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCCGCAAGT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTCAGGGTG
601 CCGGAAGATT GTTTTAA
```

```
a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGLTVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGVWRV
201 PEDCF*
```

		10	20	30	40	50	60
m601.pep		MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
a601		MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m601.pep		KIRAYGALKMGLISDVSEAAAAAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					
a601		KIRAYGALKMGLISDVSEAAAAAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					
		70	80	90	100	110	120
		130	140	150	160	170	180
m601.pep		KLHAMMGTSVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT					
a601		KLHAMMGTSVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT					
		130	140	150	160	170	180
		190	200				
m601.pep		ATKAVMSRSARVMMEGWVRVPEDCFX					
a601		ATKAVMSRSARVMMEGWVRVPEDCFX					
		190	200				

1	ATGTTGCTCC	ATCAATGCGA	CAAAGCGCGA	CATATGCGTC	CCTTTCTGCT
51	CGCGCGCGCAG	ATAAACCGTC	ATCGTCAGGC	GAGCAACCGT	GGATTGTTGT
101	CCTTCGCGGG	TTTTCGAGGGT	AATCGGGAAG	CGCAGGCTCT	TAATGCCGAC
151	CTGATTGATC	GGCAGGTTGC	GCAAATCTCT	GCTGGATTGC	AACTGTGCAA
201	TGGCGTTTCA	TCGTTGTTTG	TCCTTAATAT	TCAGATAATT	ATTGAGATTG
251	TGTATTTGTA	TGGCAGGcag	atgcgctctg	aAAaaacgct	gtcgccCGCC
301	TGCCTGCAAA	Tgcgagatta	TATCACTTGC	TTTtggcgGC	TGCATTGA

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

1 MLLHQCDKAR HMRPFLGGQ INRHQASNR GLCSFGGFQG NREAQVFNAD
51 LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>>:

1	ATGTTGCTCC	ATCAATGCGA	CAAAACGCGA	CATATGCGTC	CCCTTCTGCT
51	CAGCAGGCGA	GTA AACCGTG	ATGGTTCAGAC	GGGCAATGGT	GGATCTGGATG
101	CTTCTCTGCG	TTTGACGGGT	AATCGGAAAG	CGCAGGTCCTT	TGATACCCGAC
151	CTGATTGATC	GGCAGATTGC	GCAAAATCTCG	GCTGGATTGC	ACGCTGCGAA
201	TAGTGTTTCAT	GAGTGTGTTT	TCCTTAATAT	TCATGTAAAT	GTTGAGATGT
251	GTGCATGGTA	TGGCGTTTCC	CCCGGGGAAT	ATACCGTCAA	TCTGCAAATG
301	CGAGATTATA	TCACCTGCCT	TTAGACGCTG	CATTGA	

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```

1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*

```

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

1	ATGTTGCTCC	ATCAATGCGA	CAAAGCGCGA	CATATGCGTA	CCCTTCTGCT
51	CGGCAGGCAG	GTAACCGTC	ATGGTCAGAC	GGGCAACTGT	GGACTGGATG
101	CCTTCTGCAG	TTTGCAGGGT	AATCGGAAAG	CGCAGGTCTT	TGATACCGAC
151	CTGATTGATC	GGCAGATTGC	GCAAATCTCG	GCTGGATTGC	ACGTCTGCAA
201	TAGTGTTCAT	GAGTTGTTTT	TCCTTAATAT	TCATGTAATT	GTTGAGATGT
251	GTGCATGGTA	TGGCGTTTCC	ACCGGGGAAT	ATACCGTCAA	TCTGCAAATG
301	CGAGATTATA	TCACTCGCTT	TTAGCAGCTG	CATTGA	

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

1 MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGS TGEYTVNLQM
101 RDYITRF*OL H*

m602/a602 95.5% identity in 111 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRTLLLRQVNRHGQTGNCLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITREFXQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITREFXQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TCGTCAGTT CATCGCTCAA
201 AGGCGCGCTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGAACGCCTT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCACGGCG GCGAAAAATA TCACGAGTCC
451 GTCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCCTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGAATGGG TACACGTTGC GCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGCGCGCGC CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGCTACGGCA ATTCGGGCAT
1251 TATCAGCCCC ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GAACTGCCCG AACTTGCCCG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPNANISIL AAQEHFPGLP NVGVMDTSFH
201 QTMPEYATY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPN DCRTLLEIAD EGREGARLAL
351 EVMTCLRAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYNGSGIISP TDSSPAVLVV PTNEELMIAC DTAEAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTGACACGA CCCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

```

301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351 GGTGGGTATG CTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401 TCAAAGCCAT CGGCCACCGC ATCGCCACAG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTTGCCGCAC
551 AGGAACATTT CCCCAGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACACGT TGCGGCGACA TCGATCCGGG CGTATACAGC
901 TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951 GAACAAAAAA TCAGGTTTGC TCGGTATTTT CGAACTTTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GGCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 CATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGC CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

```

m603.pep
  1 LSSRRRGRNNDRKCGIRFAQ RGRCLKHLAPD VCFSDDDPTL KKQPQTTRRN
 51 IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCGLGERLTT PEAVITFNKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPGL PNVGVMDSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVCGG GVDALVFTGG IGENSRNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

          10      20      30      40      50      60
m603.pep  LSSRRRGRNNDRKCGIRFAQRGRCLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
          ::||| ||| :| ||||| ||||| ||| :| ||| :| ||||| ||||| |||||
g603      MDSRLRG-NDARKYGRFAQRGRCLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
          10      20      30      40      50

          70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKQVPLSGRNCHAGAVGM
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      NCVSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFNKDGNKQVPLSGRNCHAGAVGM
          60      70      80      90      100     110

          130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHGGEKYSESVLIDQAVMDDELNACIPLAPLHNPNANISGI
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      LLNELEKHGLHDRIKAIGHRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHNPNANISGI
          120     130     140     150     160     170

          190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDSFHTQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


957

```

g603      LAAQEHFPLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISLSNDCRTLEIAADEGHEGARLALAEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISLPNDCRTLEIAADEGREGARLALAEVMTCLRAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGTCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTAGACGA CCCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAACGTC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCGG TGCCTACACT TATGCCGTGC CGCGCAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCC CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGTTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGCGGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CCGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRCLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSLGLERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPANISGI LAAQEHFPL PNVGVMDSF

```

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

m603.pep	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRNIMSDQLILVL					
a603	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRNIMSDQLILVL					
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDG NKQVPLSGRNCHAGAVGM					
a603	70	80	90	100	110	120
	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDG NKQVPLSGRNCHAGAVGM					
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHGGEKYSV LIDQAVMDELNACIPLAPLHNPANISGI					
a603	130	140	150	160	170	180
	LLNELEKHELHDRIQAVGHRIAHGGEKYSV LIDQAVMDELNACIPLAPLHNPANISGI					
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSF HQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
a603	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSF HQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	250	260	270	280	290	300
	ACILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	310	320	330	340	350	360
	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
m603.pep	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELAGILX					
a603	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELVGILX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GCGGGGTTTC GGCGTGCGCG CGCGGGCGGC GGCTTCGGAT

g604 . pep

m604.seq

m604 . pep

m604/q604

a604.seq

BNSDOCID: <WO_9957280A2_1>

```

201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTACAGGAA AACGGTCGGA
401 ATGCCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
  1 MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
 51 IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI KFDLYFGCRE RYAVELKIAC FQNCVAVLHRY
201 MGNNGFADV LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA					
	70	80	90	100	110	120
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVAVLHRYMGNNGFADVFLPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
  1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGAA
 51 AATCGCCGCG GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgcca agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAAC TA CGCgcCAAC GCAGGCAAAT CCGCGGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

```

```

951 CAACGACGAC CGCTTTGCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCGG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCGtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MITEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIIIEGFF
251 GQEIHTTYN LARMNMFHVN VYNKPHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPFI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLKSHKNDT DIQFIDASGF FKKETNNNLV TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCGGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGTGCCAAAC GCAGGCAAAT CCGGCGGCGA ATTTTACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CCGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCC CCGCAGGCGT ACTTGCCCGG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MITEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFEN HHIDLFGBAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEIHNHTTYN LARMNMFLHN VNYNQFHIEL GDTLTNPKLK DSKPFDIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.pep	MMTEMQRAQLHRQIWKIADEV	RGAVD	GWDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
g605	MMTEMQRAQLHRQIWKIADEV	RGAVD	GWDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS			
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS			
m605.pep	GYPSEQDIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFENHHIDLFGBAY	
g605	GYPSEQGIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFEDHRIDLFGDAY	
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLOAKKQF			
g605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLOAKKQF			
m605.pep	DEHIEEGFFGQEIHNHTTYNLARMNMFLHN	VNYNQFHIELGDTLTNPKLK	DSKPFDIVS	
g605	DEHIEEGFFGQEIHNHTTYNLARMNMFLHN	VNYNKFHIELGDTLTNPKLK	DSKPFDIVS	
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRG	RAAIVSFPGI		
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRG	RAAIVSFPGI		
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF			
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF			
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVP	PHIAQNAAQQT	VKDNGYNLAVSSYVEAEDTRE	
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP	PHIAQNAAQQT	VKDNGYNLAVSSYVEAEDTRE	

963

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : : : :					
g605	VIDIRQLNAEISSETVAKIERLRREIDEVIAEIEYX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1  ATGATGACCG AAATACAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT AAAAGGCGTG GCGGAACTCG ATTTCCGGCAG
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACCTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTAAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGCCTGCTCT
701 TGCAAGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAAATCCA CATCGAATTG GCGACACAC
851 TGACCAATCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTTTCC
901 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CTGCAGGCGT ACTCGCCCGG AAATCCAAAG
1001 CCGATTTTGC CTTTATTCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CCGCGCCGCCA TCGTCTCATT CCCCAGGCAT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA
1151 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AGCGGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTTG AACC CGAAGA CACCCGCGAA ATTATCGACA
1451 TCAAACAGCT TAACGCCGAA ATCAGCGAAA CCGTTGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```

a605.pep
1  MMTEIQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51  YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQDIK LFDDFDFTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMFLHN VYNKFHIEL GDTLTNPKLK DSKPFDAVVS
301 NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNNGYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA EIEA*

```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQRQLHRQIWKIAD EVRGAVDGWD FKQYVLGTLFYRFISENFTD YMQAGDSSID					
	: : : : : :					
a605	MMTEIQQRAQLHRQIWKIAD EVRGAVDGWD FKQYVLGTLFYRFISENFTD YMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKV KGYFIYPGQLFCNIAAEAHQ NEELNTKLKE IFTAIESSAS					

```

a605      |||||
YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
          70      80      90      100     110     120

m605.pep      130      140      150      160      170      180
GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGNFENHHIDLFGDAY
a605      |||||
GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGSFEDHHIDLFGDAY
          130      140      150      160      170      180

m605.pep      190      200      210      220      230      240
EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF
a605      |||||
EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF
          190      200      210      220      230      240

m605.pep      250      260      270      280      290      300
DEHIIIEGFFGQEIHNHTTYNLARMNMFHNVNYNQFHIELGDTLTNPKLKDSKPFDAIVS
a605      |||||
DEHIIIEGFFGQEIHNHTTYNLARMNMFHNVNYNKFHIELGDTLTNPKLKDSKPFDAVVS
          250      260      270      280      290      300

m605.pep      310      320      330      340      350      360
NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
a605      |||||
NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
          310      320      330      340      350      360

m605.pep      370      380      390      400      410      420
FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDASGF
a605      |||||
FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDAGGF
          370      380      390      400      410      420

m605.pep      430      440      450      460      470      480
FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE
a605      |||||
FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEPEDTRE
          430      440      450      460      470      480

m605.pep      490      500      510
IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
a605      |||||
IIDIKQLNAEISETVAKIERLRREIDEVIAEIEAX
          490      500      510

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCacc ggtttgctcg accaTatgaC GCGCGACgaa gtggaagccg
251 tgTTGGCGCA CGAAATGGCG CACGTGCGCA ACGGCGACAT GGTTACGCTG
301 ACGCTGAtTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTATTTCCT AGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGCGAATACC GCGCCGAcgc
501 gggCGcggCA AACTGGTTCG GCGCACCgAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTCGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE DEAVLAHEMA HVGNGDMVTL
101 TLIQGVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGGAATACC GCGCCGATGC
501 GGGCGCGGCA AAAGTGGTCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTCGCTGGA
651 CAACCGTATC GCGCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE DEAVLAHEMA HVGNGDMVTL
101 TLIQGVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVNTFVVFLSRRIAN					
g606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVNTFVVFLSRRIAN					
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTGGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTCAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GCGCGCGGCA AACTGGTTCG GCGCGCGGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGAATC GCGCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
a606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLK TPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTL TLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTL TLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

g607.seq

```

1  ATGCTGCTCG accTgaCCG CTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTT GGCATGATTT TGATGTGGGC
351 GCGGATTACG CCGTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```

```

601 GGTTCGCGCG TGGCGACAAT GCGCGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAgccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATCCGTTT GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCTT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTACCCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFI LIAPFGEDYV AAQVVGISLS GILYMIQSV
301 GSACTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAAPWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTGTG GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGCGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAAATC
751 GCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGCGCA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTATA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

101 IWFGFLGVPF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRLHAYT SSLNRPRILIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFERSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAFAWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVPFGMVLMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLGIFGMILMWAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPRILIMLVSFAAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYASSLNRPRILIMLVSFAAFVLN					
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALGGAGCGLATMAVF WFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCVATMAVF WFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFERSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFERSPLASMYNNDDPAVL					
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTCACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTTCGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAAGTACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTCG GAAGCCAGCG CGTTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTTC GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTCC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLL TALALEMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWEGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPR LIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMPIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFERSPLV
351 SMYNNDPVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMTIH
401 AAFAWCGGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVSFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIM LVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIM LVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240
              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
              250      260      270      280      290      300
              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFERSPLVSMYNNDAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFERSPLVSMYNNDAVL
              310      320      330      340      350      360
              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIMHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIMHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420
              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMRSHKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMRSHKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacga ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LOGGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LOGGEPGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
g608	MSALLPIINRLILQSPDSRSELTSFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
g608	TFRNSAIRKILQGGEPPGAGDIRLEGDLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCT TGCCGACTGC CTCGACGAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LOGGEPGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```

m608.pep    MSALLPIINRLILQSPDSRSELAAFAGKTLTLNLAGLKLGRITDGLLSAGNGFADTEI
a608        MSALLPIINRLILQSPDSRSELAAFAGKTLTLNLAGLKLGRITDGLLSAGNGFADTEI
              10      20      30      40      50      60
              70      80      90     100     110     120
m608.pep    TFRNSAVQKILQGGEPEGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608        TFRNSAVQKILQGGEPEGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
              70      80      90     100     110     120
              130     140     150     160     170     180
m608.pep    RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608        RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
              130     140     150     160     170     180
              189
m608.pep    LERDIWIDX
a608        LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGCCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGGCCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT CATTTACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRFHIDNF LDTDFGIGSQ ADGNVRTLIM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGCCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRHIIIDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFAETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

              10      20      30      40      50      60
m609.pep    MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60
g609        MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60
              70      80      90     100     110     120
m609.pep    RLRHIIIDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
              70      80      90     100     110     120

```



```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAATCTTTGA
51  TCGCTTTGTC GGCAACTCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GAGTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAT CTTCAACTGT TGGCCGATG
351 CACCGTCTTT CATTTGCCCC GTGAGGCTGA CATCATAATC CAGTAA
```

```
a609.pep
  1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
 51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101  RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
```

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGGFFGNVFFIGAFEQAVELAA					
a609		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGGFFGNVFFIGAFEQAVELAA					
		10	20	30	40	50	60
m609.pep		70	80	90	100	110	120
		RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF					
a609		RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF					
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIIQX					
a609		HFAREADIIIIQX					
		130					

```

g510.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  ATGATTTTTC  ACGCCGCGTG  ATGCGCGAGG
101 ATATGCTGAC  CGCCGATGAT  TTGATTTATC  CGGTGTTCTG  ATTTGAGGGG
151 GCGGCGCGCG  AGGAGATGT  GCCTTCTATG  CCGGCGGTGA  AGCGTCAGAG
201 TTTGGACAGG  CTGCTGTTTA  CGCGGGAAGA  GCGCGTGAAG  CTCGGTATTC
251 CCGATGTTGG  ACTCTTTCCC  TGTTGTACGG  AAACAAAAAC  CGGGCGTCGG
301 CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  tccgagccTT
351 GCGCGAGAGG  TttccGgaac  tggggattac  gacggatgtc  gcgctcgaTc
401 cttatacggt  gcacGGTCAG  GACGGACTGA  CGGACgaaaa  cggttaCGTG
451 ATGaAtgATg  aaaCCGTAGA  AGTCTTGGTG  AAACAGGCTT  TATGCTATGC
501 AGAGCGGGCG  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GACGGGCGCG
551 TCGGCGCCAT  CCGCGAGGCT  TTGGAGGATG  CCGGACATAT  CCATACGCGG
601 ATTATGGCAT  ATTCGCCCAA  ATATGCTTCT  GCATTCTACG  GCGCCTTTCG
651 TGATGCGGTA  GGCAGTTCGG  GCAATTTGGG  AAAGGCAGAT  AAAAGACCTT
701 ATCAGATGGA  TCCTGCAAAT  ACCGATTGAG  CGCTGCATGA  AGTGGCGGCT
751 GATATTACAG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  GTTTGCGGCT

```

```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTTCGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
951 ACGTGGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep

```
1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51 AAREEDVPSM PGVKRQSLDR LLFTAEAEVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```
1 ATGATTGGAG GGCTTATGCA GTTCTCTTAC CGCAATGTTC CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAG CTGCGTATTC
251 CGATGTTGGC ACTGTTCCCG GTGTTACGG CAAACAAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCACTG TCCGCGCCTT
351 GCGCGAGAGG TTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCCTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
951 ACGTGGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```
1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51 SAREEDVPSM PGVKRQSLDR LLFTAEAEVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AOVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
m610.pep	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEAEVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGOGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM					
g610	FPELGIMTDVALDPYTVHGOGLTDENGYVMNDETVEVLVKQALCHAEAGTQVAPSDMM					
	130	140	150	160	170	180
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					
g610	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					

975

```

g610      DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAAGDILTYAIEAAKMLKRKX
           |||||
g610      GWLDGGKVVLESLLAFKRAAGDILTYAIEAAKMLKRKX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CCGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGCT GCACGGTCAG GACGGGCTGA CGGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGCGGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTGGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY RNVASARMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIARE LEDAGHIHTR
201 IMAYSAYAS AFYGPFRDAV GSSGNLGKAD KKTQYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV ELLAFKRAAG ADGILTYYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```

```

m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQVVAPSDMM
|||||
a610          FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQVVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
|||||
a610          DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
|||||
a610          TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
a610          GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCTGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTtTc cagtacctgA
251 TcgcgGTCta tggtttcCCA ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTGA ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTCTCGGAA
401 ATGTTTTCGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gCTCAtgcCG TAGCGCGTTA
501 CCATTTTCGCG TGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAVYGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCTGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGCG TTTTCATCGA GGATTTGTGA GGCAACCTGA TATTGCTCGT
351 CCAAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGCG AACGGgttac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep    MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611        MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep    LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611        LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep    ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
g611        ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep    X
g611        X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTG TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTGCGC CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFL
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

              10      20      30      40      50      60
m611.pep    MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611        MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep    LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611        LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep    ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
a611        ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
              130     140     150     160     170     180

m611.pep    X

```

a611

X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq

```

1 ATGGGgcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51 AGCCTttgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep

```

1 MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq

```

1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTTAA TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep

```

1 MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*

```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVIN TAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVG NFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq

```

1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTT.TT.AC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVFDGFR DDAVRHSGVI NTAVACLHIV
51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101 NPYXKLNKSK SPDIFRFFFX GHSN*

m612/a612 96.0% identity in 124 aa overlap

      10      20      30      40      50      60
m612.pep  MGFGGNIAKKLAGVDEIAFNFDGIVFDGFRDDAVRHSGVINTAVACLHIVGEVFADKAVE
a612      MGFGGNIAKKLAGVDEIAFDGIVFDGFRDDAVRHSGVINTAVACLHIVGKVFADKAVE
      10      20      30      40      50      60

      70      80      90     100     110     120
m612.pep  KCAENVLFKVPAlHRAAYFVGNFNPLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFFX
a612      KCAENVLFEVPAIHRAAYFVGNFNPLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRFFFX
      70      80      90     100     110     120

m612.pep  GHSNX
a612      GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCGT CGAggcagtc ggcaagggct tcgttgccgg
101 tgtttGcgGA CTCGGGTTCG CGGAAAATC CGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgtgcc
201 gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTTCG
301 CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351 CCGTATCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601 ATTTTACAGG CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151 AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201 ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTTTCGGA CTCGGATTTC CGGAAAATC CGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT

```

m613.pep

1	MSRSSRSRRS	LRRSTPSRSL	LISSRQARS	SLPMFADSDS	<u>RENPFICSAM</u>
51	<u>FLPICLMPCP</u>	MSAARLPMSA	CVPKIRANSS	DRERRRLRSP	DSTAMPRRMS
101	<u>PSSPMSPAPG</u>	SPPWRIFCTA	LLRKVISVSA	KPFPAESKPS	SVMRPAASFSP
151	AMFRVSVLPA	KAASSERLSG	LCRIRRLMMG	RRADIFSDRG	GECLLLLLPL
201	ILQA*				

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

```

      10      20      30      40      50      60
m613.pep  MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
          |||||:|||||
g613      MSRSSLRRLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP
          10      20      30      40      50      60

      70      80      90      100     110     120
m613.pep  MSAARLPMSACVPKIRANSSDARERRLPSTDAMPSPMRSPSSPMSPAPGSPWRFCTA
          ||:|||||
g613      MSVARLPMPACVPKIRANSSDARERRLPSTDAMPSPMRSPSSLMSPAPGSPWRFRIA
          70      80      90      100     110     120

```


981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1   ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTTCG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTCGCGGA CTCGGGTTTC CGGGAATATC TGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCCTGC TGGCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCACCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCGAGG TCAGGCGGTT GATGATGGGG AGGAGGCGCG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGACGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

a613.pep	1	MSRSSRSRRS	LRRSTPSRSL	LISSRQSARA	SLPMFADSGS	RENLPICSAM
	51	FLPICLMPCP	MSAARLPMSA	CVPKIRANSS	DARERRLPSR	DSTAMPRMRS
	101	PSSPMSPAPG	SPPWRIFCTA	LLRKVISVSA	KPFPAESKPS	SVMRPASFPN
	151	AMFRVSVLPA	KAASSERLSG	LCRIRRLMMG	RRADIFSDRG	GECLLLLLTL
	201	ILQA*				
m613/a613	98.0% identity in 204 aa overlap					
	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPSPAPGSPPWRICTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPSPAPGSPPWRICTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acggggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGATG ACAACCTGAT
201 TCAAACCCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGACTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCgcta
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTT CGGTTCCGAT TTTGTGAAA TGTTCTCGG
651 TGTCCGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTctaaAAA AGTGCcttTG gacgaATCTg
1001 tggATTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtc cggcgcgat
1051 tTggcgaaac tggTcaacga agccccctg tttgccggcc gccgcaacaa
1101 agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIQTL LKNKVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTPTGFSAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
201 TAAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGGCTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAA CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCgcta
501 TCAAAGCCTG GCGGCGCGCG TGCCGCGCGG CATCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCTCGG
651 TGTCCGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTTG ACCGCCAAGT GGTGTCCCC CTGCCGGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGTTTTTTC CGCGCGGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

```

m614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFSSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVPL LPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVTPEEKPSALAAALFYSLLPVLLLIGAWFYFMRMQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPEEKPSALTALFYSLLPVLLLIGAWFYFMRMQAGGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAGEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAGEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTGPFGSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQXLNVHSHKKVPLDESVDLLSLARGTGPFGSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201 TAAAAACTG CTCGACAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

```
301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGCGAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```
a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGK AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAAGEAG
201 VPPFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFTNA
          |||||
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGK
          |||||
a614      PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGK
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
          |||||
a614      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTLLAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          |||||
a614      AGSPGTGKTLLAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          |||||
a614      DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGT GPGFSGADLANLVNEAAL
          |||||
a614      GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDKSVDLLSLARGT GPGFSGADLANLVNEAAL
```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGga  ATTTGCGcCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCgcgcgtc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtggcC  GATGCCGAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCGGTTGTGT  CgcCGTtgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAGCCC  GCATTGTGGC  GGGTCTGTTT
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTgttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggtCtgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTTCGATCA  CAGCGGGCGG  TACACTTCGA  TCGGGTCGCC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKCRKLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRR  FRARFVQDVA  DDEAVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVSVAVAEAE  FEFDPsARDV  EFVVDDEDFE  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEEEFFKRS  LPFPQRFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECGLK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAA  GCGGTTGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151 AGGCGCAGGA  ATTTTCCGCC  GCGTGC GGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCCGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGGTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTTCATGAA
751 CGTGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGGCGG TACACTTCGA TGGCGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFP PRAA SISQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAAAE FEFDP SAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEFFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGK	PQCGKQAEAVARQLHA	SSSHVWQILD	RRRNLP	PRAA	
m615.pep	70	80	90	100	110	120
	SISQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIW	KSGTCRLKGL		
g615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHS	YSRKSRVSSMTGMDSVWIS	CLSSFM	TVRIRKSGK	CR	RLKGL
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSIC	RRCXRTGFVQDIA	DDEVAVARVA		
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSIC	RRCFRFRFVQDVAD	DEVAVAGVA		
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVF	QAVVSAAAAEF	FDPSAGNVEFVVDDEDF	GFDFVELCKR		
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVF	QAVVSAAAAEF	FDPSARDVEFVVDDEDF	GFDFVELCKR		
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVA	VGQGGTG DFAEEFFFKXS	LPFPRQFVEE	PKTRIVACLF		
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIA	VGQGGAGNFAEEFFFKR	SLPFPRQFVEE	PKARIVAGLF		
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVX HDI	FRVSVECC LKASDGMVILL	DFERVCGALLWGR	STAGGTLR		
g615	310	320	330	340	350	360
	VFFARVAQADNHFCVRHDI	FRVSVECC LKASDGMVILL	DFERVCGALLWGR	STAGGTLR		
m615.pep	370					
	CGRRRAAACRLX					
g615	370					
	CGRRRAAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGGGCGGCG CCGTGTCCGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTCCGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCCGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTA CTG GGTGTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCA TCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCA TSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDP SAGNV EFVVDDEFF GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTG DFA EEEEEFFK*S LPFRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRG	FGFSFEKQ	XVNAACKP	QCREQDKA	VAWQIHAC	SSSSHVW
a615	MRKRRRRG	VGSFEEQR	IDAAGKPK	QCGKQAE	AVARQLHA	ASSSSHV
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAI	SSAEGASS	MLHSXSRK	SRVSSMTG	MDSVWISC	LSSVMTV
a615	SMSRHCA	TSSADGAS	SM LHSY	SRKSRV	SSMTGM	DSVWISC
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLL	CRKRVASS	HLPARMSG	MACRDLAT	ASSICRRX	RTGFVQD
a615	QTASGHLL	CRKRVASS	HLPARMSG	MACRDLAT	ASSICRRX	FRTGFVQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVI	VCRAEFCL	NV FQAVV	SAVAAAE	FEFDP	SAGNV
a615	DAEAQAVI	VCRAEFCL	NV FQAVV	STVAAAE	FEFDP	SAGNV
	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDCVXHDFRVSVECCCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       VFFARVAQADNHFDCVXHDFRVSVECCCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||:||||:
a615       CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGGCGAT GTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGCGGCT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TCGCCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGagcaccg Ccggcaaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gcTTCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGaaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCAccgt ccgccgaaga
751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgCAA CCgcttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCG CGCCGTTTCC
951 ACATTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFGE
51  VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIPKE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRRI PAGRTRHFR QMGRGNALPA QQIIQCRLKP
201 FOTAFSRFPY PSHERTQAA YPNIHPRHR RNPRFPVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QILFLAKAFK TGKLPIPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CGCCCTGCC CGACGGCGAC GTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAG TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

```



```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTACAGCGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTGTC TCTACGAATG CAGCATAGAC GATGCCCCCT CGCCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTGCGCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSGQVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGNGHGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRRI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPILRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQVAALAAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
g616	VWLLKPATFMNRSGQVAALAAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTDYYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGVLNKPSEAPPANRRRCRRQIPAGRTRHHFR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRRNPRFPALRM					
g616	QMGRGNALPAQIIQCRLKPFQTAFSRFPYPNSHRTQAAYPNGIHPRHRRNPRFPVARM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCPILRRNCRRLARYAGTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRSTVRRRSGTMRHTCRRQIPAPVONLPNVAGRGGGKMLPRNRFILLSALWFAGG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAADTAPPPPHFDKAAHLALFFAQILFLAKAFKLGKLPYPYRSLIAFAFCFAV					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

a616.seq

```

1   ATGTCAAACA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCGTG CTACCCGTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTCATG AACCCTTCGG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGGCCTCGG CATCGGCCAC CCGGCGGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACG CATGTTCCCG ATTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTGTC GTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATGTGTTT TGCCTGCGGC
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGGAAGAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTGCGCGATA
1151 TGGCAGGTAC GGTCTCTGCA CTCTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1   MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTA YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLLTKAFK TGKLPYPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
a616	VWLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTAAYRLRLGIGHPGDRNLVVGYNLKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTAAYRLRLGIGHPGDRNLVVGYNLKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPALRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

```

m616.pep      QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPD MAXRGTSMNLPNRNFILLSALWFAGS
              |||| :||| :|||: ||||:||||:|:|:| | | :|:|||| | ||||| |||:
a616          QHRRRTIRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRGGMKLPNRNFSLLSALWFAGG
              250      260      270      280      290      300

              310      320      330      340      350      360
m616.pep      IYSLLFKAAETAPPPFP HFDKVAHLALFFAQIWLLTKAFRTDNRPIPYRSLMVFALCFAL
              ||||| |||:| ||||| |||:| ||||| |||:| ||||| |||:| ||||| |||:|
a616          IYSLLFKAADTAPPPFP HFDKAAHLALFFAQIWLLTKAFKLGKLPYRSLMVFALCFAL
              310      320      330      340      350      360

              370      380      390      400
m616.pep      FSECAQAWFTATRTGSLG DVLADLTGAALALFTARAACRPDX
              ||||| |||:| ||||| |||:| ||||| |||:| ||||| |||:|
a616          FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
              370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCGGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCTCAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301 GCGGTGGGCT ATAcacccct gccgttgacg gGCAAAATTCG GCTTTGAACT
351 GGTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTGCGCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG
751 GTAGACTTTT TCGGGCTTCT CGCCGCTTCG CTTGCCAACC ACTTTTCCc
801 gtCCGTGCGC CATTCCGTCC GCCTGCCgat gacggtttGC gtcgGcggCA
851 TCCTCTTGgt cggCggacaA ACCGTATTTC AACACTTCTT GGGCATGgAa
901 gCggTATTAA GCGTGGTGGt cgAATTTGCG ggcggactcG TTTTCCTCTA
951 TCTCGTTTAA AAACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFOT LTNNPILTPS ILGFDSL YVF LQTLVFTFG
101 GVGYTSPLPT GKFGFELVVM MGGSLLLFYT LIRQGGRLDP HMLIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVRSELLG GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGF
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCTCG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCTCAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGT TACGTTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
351 GGTCTGCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTGTCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 CTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTGCGCCCG
751 GTAAGCTTTT TCGGGCTTCT CGCCGCTTCG CTTGCCAACC ACTTTTCCc
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTTC AACACCTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTGCCC GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep

1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LOTLLVFTFG
 101 GVGYSPLPT GKFGFELVVM MGSLLLFYT LIKQGGDLS RMILIGVIFG
 151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLV KHKX*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGVGYSPLPTGKFGFELVVM					
g619	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGVGYSPLPTGKFGFELVVM					
m619.pep	130	140	150	160	170	180
	MGSLLLFYTLIKQGGDLSRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
g619	130	140	150	160	170	180
	MGSLLLFYTILIRQGGDLPMLIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	190	200	210	220	230	240
	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVKHKX					
g619	310	320				
	AVLSVVVEFAGGLVFLYLVKHKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq

1 ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTCGC CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGCGCTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTCG ATTTTGCGTT
 251 TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAAC
 351 GGTCTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGGCGGGCG CGATTTGCCG CGTATGATT TAATCGCGCT GATTTTCGGG
 451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
 501 AGAATTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGCCCCG

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751 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCC AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTTCG GCGGACTCG TTTCTCTCTA
951 TCTCGTTTAA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLIVF LQTLIVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLLFYT LIKQGGRLP RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

10 20 30 40 50 60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
|||||
a619 MPSEKNIGFMAGSSRPLWVAFALLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
10 20 30 40 50 60

70 80 90 100 110 120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLIVFTFGGVGYASLPLTGKFGFELVVM
|||||
a619 VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLIVFTFGGVGYASLPLTGKFGFELVVM
70 80 90 100 110 120

130 140 150 160 170 180
m619.pep MGSLLLLFYTLIKQGGRLDSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
|||||
a619 MGSLLLLFYTLIKQGGRLDPRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
130 140 150 160 170 180

190 200 210 220 230 240
m619.pep NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
|||||
a619 NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
190 200 210 220 230 240

250 260 270 280 290 300
m619.pep VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
|||||
a619 VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
250 260 270 280 290 300

310 320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKKX
|||||
a619 AVLSVVVEFAGGLVFLYLVLRHKKX
310 320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gttttgcct TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

g620.pep
 1 MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWID AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDA YIFK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

m620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
 451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620.pep
 1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
m620.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
m620.pep	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDPTIYIFKX					
g620	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIYIFKX					
	130	140	150	160		
m620.pep	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDPTIYIFKX					
g620	GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

a620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
 451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

a620.pep
 1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLT	EHNGPKAQIFLNGKP		
a620	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLT	EHNGPKAQIFLNGKP		
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMF	GYTKLPEEPK	GIRVIYVTD	MGNVTDW	TNP	NADTEWMDAKKAFYVIDS
a620	DQPVWFSTIKQMF	GYTKLPEEPK	GIRVIYVTD	MGNVTDW	TNP	NADTEWMDAKKAFYVIDS
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMGAEDALP	FGNKEQAEKFA	KDKGKVVGF	DDMPDTYIFKX		
a620	GFIGGMGAEDALP	FGNKEQAEKFA	KDKGKVVGF	DDMPDTYIFKX		
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAaag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCC  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTTGCCTGC
301 GGCTTGGAAT  CGATGGTTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTTG  CTAAGAAAGT  CCGTACCGAT
451 ACCGCTGTGC  GCGAAAATTC  GGTTCGATG  GCTTCCGCGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCCAGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTCCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCGAGCCAG
751 CTTCCGATAG  TCGGCAAGAG  CATGGTCGAA  CGCGCATGTA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTCATG  TTGACTTGCG  CGTGCCGCGC  GATATTGAAG
851 CGGAAGTCGG  GATTGTAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCAACATCG  TCCAAAGCGg  caaggaggca  aggcagaaag  ccgcccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTTGTC  AGGCAGCAGC
1001 AGGGCAGGCA  GagcgttcCG  CTGATTAAGG  CCTTGCGGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAAATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaaCGGCG  GAAGaggttt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGAt  tatcatttGG  ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGQIKDAV  RAAQEQESMG  AKLNALFKQT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEQ  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQRQSMP  LFMLDLAVPR  DIEAEVGDLN  DAYLYTVDDM
301 VNIQSGSKEA  RQKAAAAAET  LVSEKVAEFV  RQQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLRLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTGCG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCTAAA  GCCGTCGCGA
101 ATCTTGCCCC  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCGG  CGTCGCTGTC

```

```
301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCATG GCTTCCGCTT CCGTCAAATT
501 GCGGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCCACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATGC TTGATTGGC AGTGCCGCGT GACATTGAAG
851 CGGAAGTCGG CGATTTGAAT GATGCCATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```
1  MQLTAVGLNH OTAPLSIREK LAFAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPVVGKGMVE RALKQROSMPL FMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHOTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHOTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	130	140	150	160	170	180
	RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLTMVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CCGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACCT GGTTCCTCAT GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTGAAC GATGCCATATC TTTATACGGT GGACGATATG
901 GTCATATATC TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAACLP EAVRNLAARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

10 20 30 40 50 60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLAARSNAATEAVILSTCNRTELYCVGD
a622 MQLTAVGLNHQTAPLSIREKLAFAAAACLP EAVRNLAARSNAATEAVILSTCNRTELYCVGD
10 20 30 40 50 60

70 80 90 100 110 120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
a622 SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
70 80 90 100 110 120

130 140 150 160 170 180
m622.pep RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
a622 RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130 140 150 160 170 180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLFPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLFPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTCGTC CGCTGTTGCC GACCACGCCG TTCGTAATAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatctTTtgg CattTTCCCC aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTGTGcAcC ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
51  TATCATCGGC ATTTTTCGTC CGCTGTTGCC GACCACGCCG TTCGTAATGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTGTGCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g624          HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1   ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51  TATCATCGGC ATTTTGTTCG CGCTGTTGCC GACCACGCCG TTCGTAAGTC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
301 GTTTCATCGG TTTTGTGTTT CCTTGTCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1   MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1   ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1   atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtctTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1   MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA

```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGCG AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAATGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCGGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCAACATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCCTG TTTCAATcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gCAACgcac cgaactTCAT

1001

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501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGcCg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT
601 ACCCTcgtCT TTTTcgTttt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
  51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTCATTGCG TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10      20      30      40      50      60
m627.pep  MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||
g627      MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGPLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1   ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTG TTTTATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1   MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTGAGCGGCG TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNTNRP
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRP
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRL	NTNRPRLK	SSAASLIM	
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHT	WILRSVRLN	TNRPRLK	SSAASLMM	
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGS	SASTAGILLN	GRVRSVHKPD	WIRLRRTSS	PLKFASASGA	
g628	TVGSAASGLVSIALTKMANGS	SASTAGILLN	GRVRSVHKPD	XIRLRRTFS	LLNFASASGT	
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

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```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPPNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVHKP
101 DWIRLRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS					
a628	MCVPLKPAGCGPPNSCVSMLAAFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSI					
a628	TTGSAASGLVSI					

```

m628.pep  X
          |
a628      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggtatTGTTT  GCCGTCAGcc  tGtcggTCGG  cattgccgaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCA  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGGAtgatt  atgcagATTC  TGATGCGCAA  CcgtTTTGTC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGt  gcgGCTTTGG  GTttgtctct  gAtgtccctg
301 ctgctgcctg  CcgcGccgct  gccggtcaAA  ATGTCGGtag  Cgcctgttgc
351 CGCGCTGATC  GGGATGTTGG  tctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatGTg  ccgCTGGTGG  Gg.ttATTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCGACGTT  TGTCGCGTAT  GAGTTTGAGA  TGCTGCAAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GGCGGTTTGG  CGGTGTTTGC  CTACCTGATT
601 GCCGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGGTGA  GCGTGAATTT
651 GGGTTTGAAC  CGGACGGCGG  TGTGTGGTC  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGGTCG  GCAATATTCC  GTTATCGGG
751 CTGGTCGTGC  CGAATATCGT  CAGCCGCCTG  ATGGGCGACA  GGCTGCGCCA
801 AAGCCTGCCT  GCGGTCGCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTTGGTG  TGTTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTGAGGAA
951 ACCCGCTAT  GCCGCTGTA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKPFSLNL  ANLLLPVLF  AVLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTFAIVLT  GASIAVAGMI  MQILMRNRFV  EPSMAGAGQS  AALGILLMSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

```


m629.seq

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pap

1	<u>MTAKPFSLNL</u>	<u>TNLLLLAVLF</u>	<u>AVSLSVGVD</u>	<u>FRWSDVFSLS</u>	<u>DSQQVMFISR</u>
51	<u>LPRTFAIVLT</u>	<u>GASMAVAGMI</u>	<u>MQILMRNRFV</u>	<u>EPSMVGASQS</u>	<u>AALGLLLMTL</u>
101	<u>LLPFAAPLPAK</u>	<u>MSVAAVAALI</u>	<u>GMLVFMLLR</u>	<u>RLRPVTAQLMV</u>	<u>PLVGIIFFGV</u>
151	<u>IEAVTFIAY</u>	<u>ENEMQLMGV</u>	<u>WQQDFSSVL</u>	<u>LRGYELLWIT</u>	<u>GGLVAFYALI</u>
201	<u>ADRLTILGLG</u>	<u>ETVSNLGLN</u>	<u>RTAVLWSGLI</u>	<u>IVALITSLVI</u>	<u>VTVGNIPFIG</u>
251	<u>LVPVNIISRL</u>	<u>MGDRLLRQSL</u>	<u>AVALLGASLV</u>	<u>LLCDIIGRVI</u>	<u>VFPFEIPVST</u>
301	<u>VFGVLGTALF</u>	<u>LWLLLRKPAY</u>	<u>AV*</u>		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

m629.pep	10	20	30	40	50	60
	MTAKPFSLNLTNLLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
g629	MTAKPFSLNLANLLLPVLF	FAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT				
	10	20	30	40	50	60
m629.pep	70	80	90	100	110	120
	GASMAVAGMIMQILMRNRFVEPSMV GASQSAALG LLLMTLLP AAPLP	PAKMSVA	AAVAALI			
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALG LLLMSLLP AAPLP	PKMSVA	AAVAALI			
	70	80	90	100	110	120
m629.pep	130	140	150	160	170	180
	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATF	FIAYENEM	LQMLGVW	QQGDFSSVL		
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATF	VAYEFEM	LQMLGVW	QQGDFSSVL		
	130	140	150	160	170	180
m629.pep	190	200	210	220	230	240
	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					

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```
g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```
a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GCGCGGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCT GATGTCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTGGACGGT
551 ATGAAGTGT GTGGGCAACG GGGATTTTGG CTTTGTGTC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTAAAGGAA
951 ACCTGCTCAT GCCGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```
a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAVAALI GMLVFMMILIR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

m629/a629  95.7% identity in 322 aa overlap

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60
           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLPAAPLPAKMSVAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLPAAPLPVKMSVAVAALI
           70      80      90      100     110     120
           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

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```
a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180
           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSIVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSIVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```
g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GCGCACAGG CATTCGGTGC CTTAACGCCG GATTtgctgc
101 aacaaagcat cgccacgac ggcaattacg ccctcgcaa cgcttgggc
151 atcaatatgt ccccgaaGc gggcgtgtTg ggcaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTATTGTG GCGgcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCGGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTtT GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg tctgacacc aaagctatgt ttgctatgca
801 cttggtacat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa.....
```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```
g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTp DLLQOSIAHD GNYALANALG
51  INNSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLfAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVtGQTIT
201 WMDAFIGKLP GSIGEVSTLa LLIGGAFIVf ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```
m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCGCCATGT TCTACGGTAT
51  GTACAACGTC GCGCGCAGG CATTCGGTGC GTTAACGCCT GATTtGCTGC
101 AACAAAAACAT CGCCAACGAC TGGCATTACG CTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTcG GACAAATGC TGTtTGCGC
201 GATTTACTTC CTGCCGATT ACGCGACTGT ATTGTtTGtG GCGGtTTCT
251 GGGAAgTTTT GTTCGCCACC GTGCGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATtG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTtT GCCCGCATCG
701 CTtCTTGCGC CATTATTGCC GCGGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTtCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
```

1008

801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCCG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
 1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVL FAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 AFLFFAYPAN LSGDAVWTA DGYSGATALA QWAAHGADGL KNAVGTQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOISIAHDGNYALANALGINMSPEAGVL					
	10	20	30	40	50	60
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVVGGFWEVL FAT VRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGGFWEVL FASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHVLVGGFAIGMLFMDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLINFIGSDTKAMFAM---HLVHGTWWKDDYHSLYIK.					
	250	260	270	280		
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGCGCACAGG CATTCGGTGC GTTAACGCCC GATTTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGC AAAATGC TGTTCCGGCG
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATGTG GCGGTTTCT
 251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCGTGCGCT GGCAGGCCGT
 451 GCCTTCTGT TCTTCGCTA CCCTGCCAAC TTGAGCGCG ATGCGGTTTG
 501 GACGCGGTT GACGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
 551 CACACGGTGC AGACGGCCTG AAAAAGCCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

1009

```

701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGTTGCG TCGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLEMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIANDWHYALANALGINMSSEAGVL					
	10	20	30	40	50	60
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
a630	GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHHLVVGGFAIGMLEMATDPVSASFTNVGKWW					
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHHLVVGGFAIGMLEMATDPVSASFTNVGKWW					
	250	260	270	280	290	300
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVVNPAYPEGMMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
a630	YGALIGVMCVLIRVVNPAYPEGMMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTCGA ACTGCGCGAG CTGTTCCGAA GACAGGGCAT AGCCTTTTCG
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGAGGA

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1010

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AACATCGGT
 401 GCAGCATTC AAGGATAAGA CAAGGCTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSQYR KMVVFVFIQI HDDGDFQLRE LFERQGIQFR
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCISQITIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGAGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIQFR
 51 FKTQIRHNAP HILKRRGHLI LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIQFRFKTQIRHNAP					
g635	MTRRRVGKQNRIAIHSQYRKVMVVFVFIQIHDDGDFQLRELFERQGIQFRFKTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLI LIQFFXHVLF RQLLPVKIVQ KRRHRSRPAG KIQILLYNIE IAPFFPTLHF					
g635	HILKRRALHFLTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG KIQILLYNIE IPPRFPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSVNNRIIVKHRCISQITIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIQFR
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep  MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNP
a635      MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNP
           10      20      30      40      50      60

           70      80      90      100     110     120
m635.pep  HILKRRGHLILLIQFFXHVLFQRLLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635      HILKRRGHLILLIQFFXHVLFQRLLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
           70      80      90      100     110     120

           130
m635.pep  DFSISNRIIVDX
a635      DFSISNRIIVDX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcccACGG
201 AAATATTGCC GCTGacttcg ctgtcgtTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGCGAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCGCCCGG
751 GCGCGGGGCA AAAATTTCGG CAAGGTGTGC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCCGGTAT GGCCGAACAA AATAAAGCAT CATCAAATG TGCTGTGTTT
951 TATAGCGAAA CCGCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETOVAEA VVFIGVVRAG
101 IGINAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWOAHG TGNGQVAERY
201 VRRVYGYGTP ALVFFDGGCT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTCT CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGSCGCG TGTACGGCTA TGGTACGCC GCTCCTGTGC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCGCCCGG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```
m638.pep
1  MIGEKFIIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNOG ARGSSFEINT GIHCGQAHTG TNGGQVAERY
201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

m638.pep      10      20      30      40      50      60
MIGEKFIIVGIIIGKYALACLVDNVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI
g638          10      20      30      40      50      60
MIGGQFIVVGIVGKNALARFVDNVVNIGIVDIVEHDALIAAADGDIVEHFEPFGKHQHI

m638.pep      70      80      90      100     110     120
AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG
g638          70      80      90      100     110     120
AHIVAHGNIAADFAVVGVIHVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRAG

m638.pep      130     140     150     160     170     180
CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRI IQNIVVFNOGARGSSFEINT
g638          130     140     150     160     170     180
RVPNGNAIALIHAQGRIADDFILAHHRIGRTMKVYAEIRI IKNIVVFNOGARGGFFEINT

m638.pep      190     200     210     220     230     240
GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA
g638          190     200     210     220     230     240
GIHCWQAHTGTGNGQVAERYVRRVYGYGTPALVPFDGCCTVGRPFNRNRFVDIKEGLIYA

m638.pep      250     260
GSQFERIARPGAGKCGIPISIIIGSX
g638          250     260
GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF

m638.pep      250     260
GSQFERIARPGAGKCGIPISIIIGSX
g638          250     260
GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```
a638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCCGCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTGTG GCGTGTGGT
301 ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGGCCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTCCAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAATAA TTATTGTGTT
501 CAATCAGGCG GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCG GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```
a638.pep
1  MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIVENOG ARGSSFEINT GIHCGQAHTG TNGGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFLIYA GSQFERIARP
```


1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVNVNIGIVDIVEH	NALIAAADGDIV	EYFEPLGKHQHI		
a638	MIGGQFIVVGIVGKNALARF	VDNVVNIGIVDIVEH	DALVAAADGDIV	KHFEPLGKHQHI		
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADF	FAVVGHVHVDGETQIAE	AVFVGVVRAGIGK	NAVPPFGNVVAD	DLRTG	
a638	AHIVAHGNIAADF	FAVVGHVHVDGETQIAE	AVFVGVVRAGIGK	NAVPPFGNIVAD	DLRAG	
	130	140	150	160	170	180
m638.pep	CVPNGNAVAALVHAQSR	VADDFILAHHRIGRT	MQIYADR	IIQNIVVFNQ	GARGSF	FEINT
a638	RVPNGNAIAALVHAQSR	VADDFILPHHRIGRT	MQIDADR	IIQNIIIVFNQ	GARGSF	FEINT
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGT	PAPVAFDGCGT	VGPRPFNRNRF	VNVKFGFIYA	
a638	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGT	PAPVSFDGCR	TVGRPFNRNRF	VDVKFGLIYA	
	250	260				
m638.pep	GSQFERIARPGAGKCGIP	SISIIGSX				
a638	GSQFERIARPGAGKCGIP	SISIIDSXW				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGGTACCG TCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGCG GCAGGCGCAG TTTCCGCGCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTTCCTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AOVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGMV LMFSERLKVF DNIAGVSRD*
151 GIMLNIVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAP FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTCCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTTC GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
301 AGCGATTGTC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CCGCGTGGTG
901 GACAGCAAA CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCGATCGG
1001 AATGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAFG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDRFAVHYM YTNDSEISGN ISVGNMGGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLVNYNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSWD NSAFDLNGDG
251 FGDSAYRENG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAFGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEVSGN					
m639-1	NGVTVWNAFGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGGYVLMFSERLKVF DNIAGVSRDXGIMLVNYNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVF DNIAGVSRDQGIMLVNYNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTA AIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSWD					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSWD					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSGDSAYRPGI IDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGI IDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```
1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTCCCCC
51  GCGGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CCGCGCCCGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAAGCG GGCAAGTCCG TTTTTCCTA CAATGCCAAC TACGATAAAC
551 TGTCGCCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAA TCCTTTATCA ACAACGAAAG
651 CCAGTCAAA TAGGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CCGCGACGGC
751 TTCGGAGACA GCGGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATATGGC GCAGGCGCAA TTTCCCGCCG TTTGCGCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCCGTTA
951 TCAGGCGATG AAGGACGGC TGCTCAAAA AGTCGAAACG CCGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG
```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```
1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSIEISG ISVGNMGMVY LMFSERLKVF DNIAGVSRDQ
151 GIMLNYVNY S DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN I IDQIIWRAP VSRLMNSPA ISIVKWAQAF PAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*
```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	70	80	90	100	110	120
a639-1.pep	NGVTVWNPAGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNPAGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	130	140	150	160	170	180
a639-1.pep	ISVGNMGMVYLMFSERLKVF DNIAGVSRDQGIMLNYVNYSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGMVYLMFSERLKVF DNIAGVSRDQGIMLNYVNYSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGF GDSAYRPNGI IDQIIWRAPVSRLMNSPAISIVKWAQAF PAVLPGGVV					
m639-1	NSAFDLNGDGF GDSAYRPNGI IDQIIWRAPVSRLMNSPAISIVKWAQAF PAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLN					
	310	320	330	340		

1	ATGATTTCATA	TAATATCAAT	ATTAAGAGT	ATCGGTATAT	CGGGGATAGC
51	TATGTCCTGT	TTTTCAATCC	GGCGTATGTC	TGCGTTTCGG	GCGCGGATAA
101	CGCGCTTTTT	TACCGCCTTT	GTCTTTTTGA	CGGcggcACT	GCCCCGTTAT
151	GcggAgcgTc	tgcctGATTT	TCTGgcgAAA	AtacAgcctT	CGGAAATTTT
201	TCCGGGTGCG	GATCGTTACG	GCAAGCCGGA	aggcAAGCCT	ATggtTGCCC
251	GCgtttACAA	AGgcgATGAG	CAGCTCGGTT	TGGTTTATAT	CACGACCGAT
301	GCGGTCAATA	CGCGCGGTTA	TTCGAGCAAA	CCGATCGATA	CGCTGATGGC
351	TTTGGCAAC	GCGGCACGA	TAGCCGGGGC	GAACCTGGTC	GATCATCACG
401	AACCGATTAT	GCTGATCGGT	ATCCCGCAAT	CGCGTGTGCA	TAAGTTTCAT
451	GACAAATATA	TCGGTCTGAA	TTTTATTAAA	AATCCGCCGA	CCCCGAGCGT
501	GGCGCCGGGC	GACATCATCA	GcggtGCGAC	TgttaCACTG	ATGGTGGTTA
551	ACGACAGCAT	CCAGCGTTCC	TACAAGGTCA	TTGCCAACCA	ATACCGTCTG
601	GGTTCGGACA	AGGCCCTTCA	GACGGCATCC	GCTTCCGATG	TTCCGGGAAGC
651	CGCGCCTGCG	TCAGAAACCC	GTCCGCGCCG	TATGGCAAAT	CCCGACAAGC
701	AGGATATTTT	GTCTTGGGAC	GAACTTTTGA	AACAAAAGGC	CGTCGGCCAT
751	CTGCATATCA	CGCTCGATCA	AATCAACAAA	CTGTTTGAGA	AAGGCGGCAA
801	GGCCGGCGTG	GCCGATCACG	CCGAACAGGG	CGATCCTGAC	GATACCTTTA
851	TTGATTTGTA	TGTTGCCTTG	GTCAGCCAGC	CTTCCATCGG	TAAAGACCTG
901	CTGGGTGAGG	ACGGCTGGGC	GCATCTGCAA	AAACGGGTGA	AACCCGGGCA
951	GCAGGCGGTT	TTGGTTGCCG	GAGAGGGCCG	TTATTCTTGG	AAAGGTTCCG
1001	GCTATGTGCG	CGGCGGTATT	TTCGACCGTA	TCGAGATGAT	TCAGGGGGAG
1051	AACAGCTTCC	GTTTATCCGA	TGCCAACAC	GAACCGCTGC	TCGAGCTGTC
1101	TGCCGCCGAT	GCGCGCGGTT	TTAAGAAGT	TTCTTGGTTT	ACCATCCCTG
1151	AAGGCGTAGC	GTTTGACGGT	GCGGAGCCGT	GGCGGCTGTA	A

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

1	MIHIISILKS	IGISGIAMSC	FSIRMSAFR	ARITAFFTAF	VFLTAALPAY
51	AERLPDFLAK	IQPSEIFPGA	DRYKGPEGKP	MVARVYKGD	QLGLVYITTD
101	AVNRTHGYSK	PIDTLMALAN	DGTIAGAKLV	DVHEPIMLIG	I PQSRVDKFI
151	DKYIGLNFIK	NPPTPSVAPG	DIISGATVTL	MVUNDISIORS	YKVIANQYRL
201	GSDKALQTAS	ASDVREAAPA	SETRPRRMAN	PDKQDILSWD	ELLKQKAVGH
251	LHITLDQINK	LFEKGGKAGV	ADHAEQGDSD	DTFIDLRYAL	VSQPSIGKSL
301	LGEDGWAHLQ	KRLKPGQAAV	LVAGEGSDP	KGSGYVVRGI	DFRIEMIQGE
351	NSFRETDAQH	ERVVELSQAAD	APRFKEVSWE	TIPEGVAFDQ	AEPWRL*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2053>:

1	ATGATT	CATA	TAATAT	CAAT	ATTAA	GAGT	ATCGGT	TATAT	CGGGG	TAGT
51	CATGTC	CTGT	TTTTCA	ATCA	AACGT	ATGTC	CGCGTT	TCGG	GCGCG	GATAA
101	CGGCGT	TTTT	TGCGC	CTTT	GTCTTT	TTGA	CGGCG	GCACT	GCCCC	GCTTA
151	GCGGAG	CGTC	TGCTGA	TATT	TCTGG	CGAAA	ATACAG	CCCT	CGGAA	ATTT
201	TCCGGG	TGCG	GACCGT	TACG	GCAAG	CCGA	AGGA	AAGC	CT	ATGGTT
251	GCGTTT	ACAA	AGGCGA	TGAG	CAGTT	TGGG	CT	TATAT	CACGA	CCGAT
301	GCGGT	CAATA	CGCGCG	GTTA	TTTCGA	CAAA	CCGATT	GATA	CGCT	GATGGT
351	GTTGGC	AAAC	GACGGC	ACGA	TAGCC	GGGG	GAAACT	TGGT	C	GACCAT
401	AACCGA	ATTAT	GCTGAT	CCGT	ATCCC	GAT	...			

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK					
	: : : : : : : : : :					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAVFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||
g640           IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||
g640           DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
               130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFLTAALPAYAERLPDFLAK
               |||||
a640           MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||
a640           IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||
a640           DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGCGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG GTTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggttT Gcacggcgctc gagCAGGGtt tggT'TTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGCGGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTGCGCGC GTTCGTAATC GACGAATCTG

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1018

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701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCGAGG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCTGCCAGT ATTTTCGCGG
1051 GttgACGTAA ATGGTTtggt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCgcgcgcg gaggtTtcggt gttcggtaAc gcccaaacgg
1151 cggcttttcgc ctTTGAAAT CATGTCCAAA CCTGTGCGA CTTGCgtctt
1201 gccgcggaac tCTTGAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVLLYED KKS GDDFADE DFLQAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVVFVQLN ACFFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVSAFKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLER QTSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGFVFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGC GGAT GTCGTT CAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTT CAGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCCG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CCGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAAACGCG GCAAACCGCG
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CCGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGA CTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTTG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CTTTGA AAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATGCGCGAA CTCTTGCA GT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADV SFQI FKDVFNHVR HADQLQAAAD KDLVLAQTG
251 SVALGEFHG GCRHFGIDAV DGVT DGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRR
351 GGFGFNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVRLYED		
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFLLYED					
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN					
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEF	LQHLRGG					
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGVWSAFKTLRAQEF	LQHLRGG					
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFV	IDEFVADVS					
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFV	IDESDIVADIS					
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRHFGIDA	VDGVT	DGA			
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRHFGIDA	VDGVT	DGA			
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRG	VDVNGLSVDI					
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRG	VDVNGL	FVGI				
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQ	HQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVTLCDLRFAAELLQRLQ	HQRAFDAGTQR					
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1   GCCTGCCGCC GTATTTGCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTCCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCGGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGC GCGGCGG CGTAAAGTGA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGC GCGCGCG
601 GATTTGCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

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1020

```
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTTCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G
```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```
a642.pep Length: 407
  1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTF
251 SVALGEFHGG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRRA
351 GGFVFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP
```

m642/a642 95.8% identity in 407 aa overlap

```
          10      20      30      40      50      60
m642.pep  ACRRICPLPAISAVQYIFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
          |||||  |||||:|||||
a642      ACRRICPLSAISAVQYVFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
          10      20      30      40      50      60

          70      80      90     100     110     120
m642.pep  LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV FVQLHACFFFFGGGADKL VVNFGIKHIV
          |||||  |||||:|||||
a642      LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLV FVQLHACFFFFGGGADKL VVNFGIKHIV
          70      80      90     100     110     120

          130     140     150     160     170     180
m642.pep  RAFKNREGADVDSDIAGGVS AFKTLRTQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
          |||||  |||||:|||||
a642      RAFKNREGADVDSDIAGGVS AFKTLRAQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
          130     140     150     160     170     180

          190     200     210     220     230     240
m642.pep  RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDV VADVSFQIFKDV FHNVRHADQLQAAAD
          |||||  |||||:|||||
a642      GRNGMADVAVKNLGNLMAAPDFAAFVIDESDV VADVSFQVFKGV FHNVRHADQLQAAAD
          190     200     210     220     230     240

          250     260     270     280     290     300
m642.pep  KDVLERAQTG SVALGEFHGGGCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
          |||||  |||||:|||||
a642      KDVLERAQTG SVALGEFHGGGCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
          250     260     270     280     290     300

          310     320     330     340     350     360
m642.pep  GEFVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGF GFGNTQT
          |||||  |||||:|||||
a642      GEFVAFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGF GFGNAXT
          310     320     330     340     350     360

          370     380     390     400
m642.pep  AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
          |||||  |||||:|||||
a642      AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
```


1022

a643.seq
 1 ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCGCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CCGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGCGCGAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCCGTTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTEMVSSACRRRLFRATSCMSSSAAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFVSX					
a643	SVAVWVSDGMAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCCGCTCG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCGGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
 201 ATTcCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAGT
 351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGTGTTG CAGCCTCTGC AAGagttcgg cggcgaagcG
 451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAagcgcaaa gccgcccgttt
 501 gggcgTtacc gaacccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgcccacaa
 651 agagcgcaaa aacGGcaaac tcgccaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
 801 GATGAAACTC TCCCGGGGCG ACGTGCCCG TTTGCGCGCG TTCCAAACA
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACCGCGCG AAATCCAACG CCGCCATCAG GTTTCCGAAA
 1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgctcg GCccgTCGCC
 1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
 1101 TTAacgCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
 1151 AACGCGGACA CCCAGCCGCG AATATCGCCA TCGATATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACACACAGTT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
 1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgett tgCCGCGGTT
 1351 GCCcgcGact ACGCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GACGCCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

1023

1451 TCGCCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYT DEQTIYVNAA
 201 KYWQGNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHRQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGIK LDKNQTLDDA VQTDVRFVA
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCGCGCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
 201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCC
 251 AAGACAATAG GCTTGCTTGA AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTACC GAACCCGAAA CCTCCGCGC GGCATTTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTCAGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCGCT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTTACCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCGAGA
 1001 TTCTTTACCG CTACGTCTGC CATTCGTTT CGCCTGTTGC CCCCCTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGTGCG AAGGGTTTG
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACAGTT
 1251 TGTCGCGCC ACCGCCAAG AAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCCCT GCTCGACCG CTGCAAACCG ATGCCGCTT TGCCGCCGTC
 1351 GCCCGGACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCGTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCCGCCGACT CTTTGTCTTC GTACAGCGCA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
 201 KYWQGNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

	10	20	30	40	50	60
	70	80	90	100	110	120
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRRKGSQFEIQEVLRI					
g644	LKHIESAFPRIFFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKHGGRRKGSQFEIQEVLRI					
	130	140	150	160	170	180
m644.pep	AGHYGVVPTLRTGIEGALVLQPLQEFGEAQAQGLEMIFKGEGGGLGVTEPETSGAAIA					
g644	AGHYGVVPTLRTGIEGALVLQPLQEFGEAQAQGLDMIFKGESRRGLGVTEPETSGAAIA					
	190	200	210	220	230	240
m644.pep	REMQSYEYIDGQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
g644	REMQSCYEYTDQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	250	260	270	280	290	300
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSLQLIGMTHGIM					
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNIIFIRSLQLIGMTHGIM					
	310	320	330	340	350	360
m644.pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMLEANIVK					
g644	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLMLEANIVK					
	370	380	390	400	410	420
m644.pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	430	440	450	460	470	480
m644.pep	TAEKEAGMKLDKNQTLTLDRLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
g644	TAEKEAGIKLDKNQTLTLDVQTDVRFVAAVARDYALPEDIRSFLQEHTLTDACALQKVFI					
	490	500	510			
m644.pep	GKIIARLFVVFVQAKHEDTAAFLNDIRKDILDCRYCGX					
g644	GKIIARLFVVFVQEEHEDTTAFLNDIRKDILDCRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTCAGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCAGAGCG ACGTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

```
851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACAGTT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```
a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYT DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFIRSRL QLIGMTHGIM
301 EYTLNLERI VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*
```

m644/a644 97.3% identity in 517 aa overlap

```

      10      20      30      40      50      60
m644.pep  MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644      MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
      10      20      30      40      50      60
m644.pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
a644      LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
      70      80      90     100     110     120
m644.pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
a644      LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
      70      80      90     100     110     120
m644.pep  AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMIKFKEGGGLGVTEPETSGAAIA
a644      AGHYGVPVXXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
      130     140     150     160     170     180
m644.pep  REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
a644      REMQSYEYTDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
      190     200     210     220     230     240
m644.pep  ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
a644      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
      250     260     270     280     290     300
m644.pep  EYILENLERIYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK
a644      EYTLNLERIYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK
      310     320     330     340     350     360
m644.pep  EYILENLERIYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK
a644      EYTLNLERIYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK
```

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVF					
a644	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVF					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATGTCG  ATGCCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACATTGA  ATCTTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCAGCG  AGTTGTCCGT  GCGCCACGCC  GATACGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTCTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAata  CTGTCTCTCC  GCGTTGAGT  TCGCGCAACA
251 CCGCTTCGCG  CACGCTGCCT  TCGCTGAACG  GTTTGACAAA  GGTTTTCACG
301 GCGAGGCGGC  GGCTCGGTGC  AGTGGTAATC  AGCGAGAAGT  CGCGCAGACC
351 TTCGAGCGCC  ATGCTGAGGG  TGGCGGAAT  CGGCGTGGCG  GTCATGGTTA
401 GGATGTCGAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGTCGCACG
451 CCGAAGCGGT  GTTCTTCATC  GATAATCAAT  AAACCTAAGT  TTTTGAATTT
501 TATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACGATA  TCGACAGTAC
551 CGTCCGCCAT  GCCTTCGAGC  GTGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CCGCAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTTCGGCGAA
651 GTTTTGCGCG  TGCTGCTCGA  CCAGAAGCGT  GGTCGGGGCG  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGCGAAG  GGCAGCTTCG
751 GTTTTGCCGA  AACCGACATC  GCCGCACACA  AGTCGGTCCA  TCGGCTTCGC
801 CTGCGTCAAA  TCTTTAATCA  CGGcgcgcat  ggcggcggc  TGGTCTTCGG
851 TTCTCTCGTA  G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMNVLALGMS  MPVSMMEQS  NTLNLCKKKS  RMTCSRSSR  SCPCATPIRA
51  SGRVSSRSR  IFSIVSTSLC  RKNTCPPLRS  SRNTASRTL  SLNGLTKVFT
101 ARRLGAVVI  SEKSRRPSSA  MLRVRGIGVA  VMVRMSTLR  RRLSCSFCRT
151 PKRCSSSIIN  KPKFLNFMSS  CTNLCPVITI  STVPSAMPSS  VALVALLLLK
201 RERLATFTGK  SAKRSKFCA  CCSTRSVVGA  STATCLPPIT  ATNAARRATS
251 VLPKPTSPHT  SRSIGFACVK  SLITAAMAAA  WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATATCG  ATACCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACGTTAA  ATCGTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCAGCG  AGTTGTCCGT  GCGCCACGCC  GATGCGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTTTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAAATA  CCTGTCTCTC  GCGTTGAGT  TCGCGCAACA
251 CCGCTTCGCG  CACGCTGCCT  TCGCTAAAGG  GTTTGACAAA  GGTTTTGACG
301 GCGAGGCGGC  GGCTGGGCGC  GGTGGTAATC  AGCGAGAAGT  CGCGCAGTCC
351 TTCCAACGCC  ATACTTAAAG  TACGCGGAAT  CGGCGTGGCG  GTCATGGTAA
401 GGATATCAAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGACGCACG
451 CCGAAGCGGT  GTTCTTCGTC  GATAATCACT  AAACCTAAGT  TTTTGAATTT
501 GATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACAATA  TCGACCGTGC
551 CGTCTGCCAT  GCCTTCAGC  GCGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CCGCAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTTCGGCGAA
651 GTTTTGCGCG  TGCTGCTCGA  CCAAAAGCGT  GGTCGGAGCA  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGCGCAG  GGCAGCTTCG
751 GTTTTGCCGA  AGCCGACATC  GCCGCACACA  AGGCGATCCA  TCGGCTTCGC
801 TTGCGTCAAA  TCTTTAATCA  CGGCGGCGAT  GCGCGCGGCC  TGGTCTTCGG

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m645 . pep

1	MMVMVLALGIS	IPVSMMEVQS	NTLNRCKKKS	RMTCSSSRSR	SCPCATPMRA
51	SGSRVSSRSR	IFSVIYSTSLC	RKNTCPPRLS	SRNASTRTLP	SLKGLTKVLT
101	ARRRLGAVVI	SEKSRSPSNA	ILKVRGIGVA	VMVRISTLAR	RLRSCSFVRT
151	PKRCSSSIIT	KPKFNLNMSS	CTSLCVPITI	STVP SA MPSS	<u>AA</u> LVALLLLLK
201	RERLATFTPG	SAKRSACFKC	CSSTSVVGVA	STATCLPPT	ATNAARRATS
251	VLPKPTSPHT	RRSIGFACVK	SLTAA MA AAA	WSSVSS*	

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMVLALGISIPVSMVVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
g645	MMVLALGMSMPVSMVVEQSNTLNLCCKKSRMTCSSSRSRSCPCATPIRASGSRVSSRSR					
	10	20	30	40	50	60
m645.pep	IFSIVSTSLCRKNCTCPPRLSSRNNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA					
g645	IFSIVSTSLCRKNCTCPPRLSSRNNTASRTLPSLNGLTKVFTARRRLGAVVISEKSRRPSSA					
	70	80	90	100	110	120
m645.pep	ILKVRGIGVAVMVRISTLARRRLLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
g645	MLRVRGIGVAVMVRMSTLARRRLLSCSFRTPKRCSSSIINKPKFLNFMSSCTNLCPVITI					
	130	140	150	160	170	180
m645.pep	STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSAKFCACCSTKSVVGASTATCLPPIT					
g645	STVPSAMPSSVALVALLLLKRERLATFTGKSAKRSAKFCACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
g645	ATNAARRATSVLPKPTSPHTSRSIGFACVKSLITAAMAAWSSVSSX					
	250	260	270	280		

a645.seq

1	ATGATGATGG	TGTTGGCGTT	GGAATGTCG	ATACCGGTTT	CGATGATGGT
51	GGAACAGAGC	AACACGTTAA	ATCGTTGCTG	CAAAAAGTCG	CGCATGACTT
101	GTTCCAGCTC	GCCTCGCGC	AGTTGTCCGT	CGGCCACGCC	GATGCGGGCT
151	TCGGGACGCA	GGGTTTCCAG	CCGCTCACGC	ATGTTTTTCGA	TGGTATCCAC
201	TTCATTGTGC	AGGAAAAATA	CTTGCCCGCC	CGGTTTGAGT	TCGCGCAATA
251	CGGCTTCGCG	CACGCTGCCT	TCGCTGAACG	GTTTGACAAA	GGTTTTGACG
301	GCGAGGCGGC	GGCTGGGCGC	AGTGGTAATC	AGCGAGAAGT	CGCGCAGTCC
351	TTCACGCGCC	ATACTAAAG	TACGCGGAAT	CGGCGTAGCG	GTCATGGTAA
401	GGATGTCGAC	ATTGGCGCGC	AGGCGTTTGA	GCTGCTCTTT	CTGACGCACG
451	CCGAAGCGGT	GTTCTTCGTC	GATAATCACT	AAACCTACGT	TTTTGAATTT
501	TATGTGCTCC	TGACCAAGTT	TGTGCGTACC	GATAACAATA	TCGACCGTGC
551	CGTCCGCCAT	GCCTTCCAGC	GCGGCTTTGG	TGGCTTTGCT	GTTGTTGAAA
601	CGCGAAAGGC	TGGGACTTT	CACGGGAAA	TCGCGGAAGC	GGTCGGCAAA
651	ATTTTGC GCG	TGCTGCTCGA	CCAGAAGCGT	GGTCGGTGCG	AGTACGGCAA
701	CTTGTTTGCC	ACCCATTACC	GCCACAAACG	CGGCGCGCAG	GGCGACTTCG
751	GTTTTCGCCA	AACCGACATC	GCCGCACACG	AGGCGGTCCA	TCGGCTTCGC
801	CTTCGTCAAA	TCTTTAATCA	CGGCGGCGAT	GGCGGCTGCC	TGGTCTTCGG
851	TTTCTTCTGA	G			

a645.pcp

1 MMMVLALGMS IPVSMMVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

1028

51 S GSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
 101 A RRRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
 151 P KRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 R ERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
 251 V LPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/a645 96.9% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
a645	MMMVLALGMSIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSSA					
a645	MFSMVSTSLCRKNTCPPLSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
a645	ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCAACCSTKSVVGASTATCLPPIT					
a645	STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCAACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
a645	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

g647.seq
 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
 251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

g647.pep
 1 MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
 51 GFKGTVGQTE RGTVAADVTV FRQIVGVDD TDAERTAVHS RGTRGFYRIS
 101 LII*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

m647.seq
 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
 251 AGCGAACGGC GGCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

m647.pep
 1 MQRLAADGIQ IFFVSVGDQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGTRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
g647	MQRLAADGIQIFFVVDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	: : : : :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq

1	GTGCAAAGGC	TCGTTACACA	CAGCGTCCAA	GTCTTTTTTG	TAGGTGTCGA
51	TGGGCAGTTT	GCCTTGCGAA	TAAACGGTTT	GGTTAAAGAG	CGTGACGCA
101	CCGTATTCTT	TGGCAAGGTT	TGCCGATGCT	TTGAGCAGGT	AATACTGTAT
151	GGCTTCAAAG	GTACGGTGGG	TCAGACCGAG	CGCGGAGCCG	TCGCTGTAGC
201	GGACACCGTT	TTTCGCCAAA	TAATACGCAT	AGTTGATCAC	GCCGATACCG
251	AGCGAACGGC	GGCCCATAGT	GGAGGTACGC	GCGGCTTCTA	CCGGATATCC
301	CTGATAATCT	AA			

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep

1	VQRLVTHSVQ	VFFVGVGDGQF	ALRINGLVKE	RARTVFFGKV	CRCFEQVILY
51	GFKGTVGQTE	RGAVAVADTV	FRQIIRIVDH	ADTERTAHS	GGTRGFYRIS
101	LII*				

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : : : : : :					
a647	VQRLVTHSVQVFFVGVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	: : : : :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq

1	ATGAACAGGC	GCAACGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGAT
51	CGACGTTTTG	AATGTAGATG	CGCCCGGTCC	CGGCACGCTC	CTGCATCAGC
101	GTGGAAAACA	GGTCGGCAGC	CGGAATGATA	CGCTTGCGTA	TGTTCCGGTC
151	TTGCTCGTAT	TCGCTATAGA	GCCGCTCAAA	TTGCTCTTGG	TCGGCAAAAA
201	ACGCTTCGTA	CAACCCCGAA	ACCTCGTTGG	GCGAAAACAG	CGTAATGTTG
251	CCGCCCTTAA	TCAGGCGGGT	GTACAGCAGG	CGGTTGATTT	GCACGCCATA
301	ATCAAGCTGG	CGGATACGGT	TGTCTTCCAC	GCCCCGGTTG	TTTTTCAACA
351	CCAGCAGGCT	TTGGGCTTCA	ATATGCCACA	AGGGGTAGAA	CAAGGTTGCC
401	GCGCCGCCGC	GCACGCCACC	TTGCGAACAA	GATTTGACCG	CCGCCTGAAA
451	CATCTTAAAG	AAGGGAATGC	AGCCGGTATG	CCGGGCTTCA	CCGCCCCGGA
501	TTTCGCTGTC	CAGCCCGCGG	ATACGTCCGG	CATTGATGCC	GATGCCCGCG
551	CGTTGGGAAA	CGTATTTTAC	AATCGCGCTG	GTAGTGGCAT	TGATGGAATC
601	CAAATATCG	TCGCATTCAA	TCAGCACACA	GCTTGA	

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHORGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCCTGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTTCACAA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCGCC TTGCGAACAG GATTTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHORGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
101 IKLDTVVVFH TAVVFQHQQA FGFDMPOGVE QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHORGKQVGSRNDAALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHORGKQVGSRNDTLAYVRVLLVFRIEPLK					
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLDTVVVFHTAVVFQHQQA					
	70	80	90	100	110	120
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVIDLHAIKLADTVVFHAPVVFQHQQA					
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
	130	140	150	160	170	180
g648	FGFNMPQGV E QGCRAAAHATLRTFRDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			
g648	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCCTGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTTCACAA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCGGGA

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1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGCA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCT TCGCATTCGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDPAGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRDARIERAVRIAVIDVLNVDPAGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRNARIERAVRIAVIDVLNVDPAGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACGTC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACGTC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
 101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VQELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX			
g649	VQELRENKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

a649.seq

1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
 51 CGTGCCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
 251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCTG CGGCAGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
 101 FRR*

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60

	70	80	90	100
m649.pep	VQELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX			
a649	VQELRENKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

g650.seq

1 ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCGGTTTG
 51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
 101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
 151 TATTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
 201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
 251 CAAGCCGCAG CTATTTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
 301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCC CCGAAGCCGC
 351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
 401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
 451 GGCTTGGAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
 501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatgga CTGTTCCGGC
 551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
 601 CGCGCCGTC AACCgcGCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
 651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
 701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTGAATCC TGCATTCAAC GTCCCGCGt tcatCCCCAA AAACaaacgc
901 aaactGCTGC TTCTGTCTGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCGggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcatt accgaaccgc ccctTGCAGC
1351 AGCCGCAGCg CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pap
1  MSKLKTIALT ASGLSVCPGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1  ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCGGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGTACCAGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGTATG CCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTAAACCC CGCATTCAAC GTCCCGCGCT TTATCCCCAA AAGCAAACGC
901 AAAGTCTGC TTCTGTCTGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pap
1  MSKLKTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKSLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKSLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGEVNPPELVRRHESKFIAHSYFNRVINRSRPFMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFMRGEVNPPELVRRHESKFIAHSYFDRVVNRSRPFMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEVNGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNI IAT					
g650	LFGDWPLAFAAYNWGEVNGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNI IAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTPYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDTPYRSNMPAGTVNVSIARIQPPAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCFYCRTPCDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTRSPCFHYRTPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

1	ATGTCCAAAC	TCAAAACCAT	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGGCAGCCT	GTGGAGCGAG	CTGCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTTCAAC	AGGGTCATCA	ACCGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTTCATGAAA	GCGCGTTCTG	CACCAAAGCC	AAATCACACG
401	TCCGGGCATC	GGGCCTGTGG	CAGTTCATGC	CCGCTACCGG	CAGGCATTAC
451	GGCCTGGAAA	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCGGCG
551	ACTGGCCGCT	CGCCTTTGCC	GCCTACAAC	GGGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCCG	CGCCCAAGGG	CTCGAACCAG	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCGCC	CCCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATTT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGGC	TTGCCGGCAT	CACGCAAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGGGT	TCATCCCCAA	AAGCAAACGC

1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```
1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*
```

m650/a650 99.1% identity in 465 aa overlap

```
10 20 30 40 50 60
m650.pep MSKLKTIALTASGLSVCPGF LYAQNTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE
|||||
a650 MSKLKTIALTASGLSVCPGF LYAQNTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWSE
10 20 30 40 50 60

70 80 90 100 110 120
m650.pep LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEAALLP
|||||
a650 LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEAALLP
70 80 90 100 110 120

130 140 150 160 170 180
m650.pep FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
|||||
a650 FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
130 140 150 160 170 180

190 200 210 220 230 240
m650.pep LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
|||||
a650 LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
190 200 210 220 230 240

250 260 270 280 290 300
m650.pep PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
|||||
a650 PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
250 260 270 280 290 300

310 320 330 340 350 360
m650.pep KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
|||||
a650 KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
310 320 330 340 350 360

370 380 390 400 410 420
m650.pep NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQQT
|||||
a650 NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQQT
```

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRXTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRXTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGCGG GCGGAAGACG TATTATTTCG ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGA GGCTTGGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGCGCACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct cggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAACccgG TTCTTTGAGc
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCCGGCAA AGCCGCATTc TACCAACTGG
1001 GCAATATA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKLLTEKL GKQVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTTCTATATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGCGG GCGGAAGACG TATTATTTCG ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGTAAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGGACT ACCCCAGCAA AGCCGCATTc TACCAACTGG
1001 GCAATATA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```



```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKKLLEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
g652           MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              |||||
g652           EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
g652           SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              |||||
g652           GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGKRVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              |||||
g652           LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAKYNQLLRIEEELAEAAADYPSKAAFYQLGKX
              |||||
g652           RSDRMAKYNQLLRIEEELAEAAAYPGKAAFYQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGCG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCCTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGCAAG TCCAACCTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GGVQVLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS					
a652	LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGKX					
a652	RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGCAGC GCGACAAATC CCGCTATTCC GGCAAAGCGC TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGCC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCCGCGA AGCGTTGCGC TCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGCTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCCG ATTATTTCCA
851 TTGAAGACCG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCGACGATC TGTTCTGAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCGGCGCAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

g652-1.pap

```
1 MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51 LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLTL
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```
1 ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51 CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTTC GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGCGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTCCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGCAGCACT TGTTCTGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 CTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCCGA CTGGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```
1 MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51 LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLTL
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*
```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRYG					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRYG					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQLVGDDLFVTNPKILAEIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGKRVQLVGDDLFVTNPKILAEIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAYYPGK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCGCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTGG GCGAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCGCCCG AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGA AGCCGAAGGC CGTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLESQ VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGGAN TLAVSMAMAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLDCSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDN NDWEGWKLLT
301 EKLGGKVLVQ GDDLFTVNP KILAEIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

              70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

              130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

              190     200     210     220     230     240
m652-1      CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLTL
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLTL
              250     260     270     280     290     300

              310     320     330     340     350     360
m652-1      EKLGGRRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGKVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

              370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
              370     380     390     400     410     420

              429
m652-1      AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

g653.seq

```

1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGct ttgcccAAG
101 CGGCttcggc ggctttgcCg gtgaTTTTCa TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCTGTGCG GCCGGAaacg atgcgCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTCACTTGT TTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGGCGC
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

g653.pep

```

1  MAAEPMRMPE VTYGFGSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

m653.seq

```

1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGGAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```
m653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
  51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
 101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
 151 TGLGYSPPAT RPA*
```

m653/g653 96.9% identity in 163 aa overlap

```
                10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
                |||||
g653          MAAEPMRMPEVTYGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
                10      20      30      40      50      60

                70      80      90     100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
                |||||:|||||
g653          MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
                70      80      90     100     110     120

                130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX
                |||||
g653          SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATSPAX
                130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```
a653.seq
  1 ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
  51 ATCATTCCGG ATGGCGTTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
 101 CAGCTTCGCG GCGTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG
 151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
 201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
 251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
 301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGGAGAGTT
 351 CAACGCTTTT TCGTGGGTAT TGTGCGGGCA CAAAATTACG CCGCCGCGAG
 401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
 451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```
a653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
  51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
 101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
 151 TGLGYSPPAT RPA*
```

m653/a653 100.0% identity in 163 aa overlap

```
                10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
                |||||
a653          MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
                10      20      30      40      50      60

                70      80      90     100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
                |||||
a653          MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
                70      80      90     100     110     120

                130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX
                |||||
a653          SWVLSRHKITPPRGPRRVLWVVVTKSQNGTGLGYSPPATRPAX
```

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```

g656.seq
  1 ATGCCGCGTT TCTCCGTTTC GATTCTTCG ATGATTTCCTA TCGCGCGGAC
 51 TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TGA CTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGCGGG GGT TTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTCGGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```

g656.pep
  1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
 51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```

m656.seq
  1 ATGCCGCGTT TGCTCGTTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
 51 TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGCG CTTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TAACTTTGAC
201 TTCGCCGGTT TTA CTTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGCGGG GGT TTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTTTCGCG TCGGACGAGG ATTCGGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```

m656.pep
  1 MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
 51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLRSRTR ISGEEPTMWK SPKS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

m656.pep	10	20	30	40	50	60
	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
g656	10	20	30	40	50	60
	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT					
m656.pep	70	80	90	100	110	120
	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
g656	70	80	90	100	110	120
	ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
m656.pep	130	140				
	ITSLRSRTRISGEEPTMWKSPKSX					
g656	130	140				
	MTSSRSRTRISGEEPTMWKSPKSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTGTTCGG TAACTTTGAC
201 TTCGCCGGTT TTA CTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGAT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCCGGCGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGACGAGG ATTTCCGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGR MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR					
	70	80	90	100	110	120
m656.pep	ITSLRSRRTRISGEEPTMWKSPKSX					
a656	MTSSRSRRTRISGEEPTMWKSPKSX					
	130	140				
m656.pep	ITSLRSRRTRISGEEPTMWKSPKSX					
a656	MTSSRSRRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGCGGGTta cgACCGAATT TGAaaacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTACAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGT GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccG CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTGGCGta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAACCGGCC CGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAAGTTCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCCttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTTCGAAAA TGGGACACTT TaccgTTTGT ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYVGV

1046

251 LAVEMFVVDG THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAAATG TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACCTCA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTGCGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCCTTG TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTAA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDPAPAAEFA
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVVCCKA EDITEASAQF LFGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADELQVGVG
 251 LAVEMFVVDG THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGE PDWL PLQSHPNHL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAM	LGILGGGQLGR	MFTVAAKTM	GYKVTVLDP	DPDPAPAAEF	ADRHLCA
	10	20	30	40	50	60
g657	MNTTPILPPAM	LGILGGGQLGR	MFAVAAKTM	GYKVTVLDP	DPDPNAPAAEF	ADRHLCA
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVVCCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAFA	EHGGVDCVL
	130	140	150	160	170	180
g657	TAPYQAVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAFA	EHGGVDCVL

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1   ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51  CGGACAATTA GGCAGAATGT TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAAC TCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTGCTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCCTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGGCCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1   MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGGKQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVDG THELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSXL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAFPND					

a657	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN	10	20	30	40	50	60
m657.pep	QAALDELA	70	80	90	100	110	120
a657	QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
m657.pep	TAPYQVVC	130	140	150	160	170	180
a657	TAPYQAICKAEDITEESIQLPGILKTATLGYDGKGQIRVKTVDLKAFAEHRGVDCVL	130	140	150	160	170	180
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR	190	200	210	220	230	240
a657	EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQQARQMAQR	190	200	210	220	230	240
m657.pep	LADEL	250	260	270	280	290	300
a657	LADELNYVGV	250	260	270	280	290	300
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPN	310	320	330	340	350	360
a657	PADTKLLSSCCMANILGDVWQEDGGEPDWFLQSRPDAHLHLYGKKT	310	320	330	340	350	360
m657.pep	TTDSDTAFQ	370	379				
a657	STDSDTAFQ	370					

g658.seq

1	ATGGTGGCCG	GAATTGTGCG	TGCGCGGGGC	GGTTTCATTG	ACGAGCAATT
51	CATGTGTGTC	GCCGACAACA	AACATTTCTA	CCGCCAatac	GCCGACATAA
101	TCCAATTTCG	CCGCCAagcG	TTGCGCCGTC	TGCCGCGCCT	GTTGCTGCAC
151	GTCGGCACTC	AGCCGCGcgg	gACGATGga	atAAGCCAAg	ATGCCGTTTT
201	CGTGGATGTT	TTCGGCGGGg	TCCAAGGTTT	GCACGTTTTT	ATCGTTCAGA
251	CGGCATACGA	TCACGGAAAT	CTCGCCGCGC	AAGTCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCCGCCGT	GTTCGGCAA	CGCGGCTTTG	AGTTCGTCCA
351	ACGTTTTGAC	GCGGATTTGA	CCTTTGCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAAA	TTGCGCGCTT	GCTTCAAGTA	TGTCTTCGGC
451	CTTGCAAACC	CCGTGATACG	GCGCGTTTGT	CAAGCTGCT	TTGCGTATCC
501	ACGCTTTTTT	CTGAATGCGG	TTTTGTGCAA	TGGACACGCA	TCGCGCGCTG
551	GGGAAACGT	TGGTATGCTT	TGCCAGAGAG	CGCATCGCGT	CGGCAAttgac
601	gtTTTCAAAT	TCGGTcgtaA	CCGCCGCGCA	TTTTGCCAAT	TCGTCCAACG
651	CGGCCCCGAT	GTCAAACGGC	GCGCACAAAT	GGCGGTCGGC	AAATTCCGCC
701	GCGGCGCGAT	TCGGGTCCGG	ATCGAGAACG	GTTACTTTGT	AGCCCATGGT
751	TTTAGCGGCA	ACGGCAAACA	TTctgcctAA		

g658.pep

1	MVAGIVRARG	GFIDEQFMCV	ADNKHFYRQY	ADIIQFVRQA	LRLRLPRLLH
51	VGTPRGDDG	<u>ISQDAVFVDV</u>	FGGVEGLHVF	IVQTAYDHGN	LAAOVHHFFO

m658.seq

1	ATGGTGTCCG	GAATTGTGCG	GGCGCGGGGC	GATTTCGTTG	ACGACCAATT
51	CATGCGTGTC	ACGACAACA	AACATTTCTA	CCGCCAATAC	GCCGACATAA
101	TCCAATTCGT	CCGCGCAAGC	TTGCGCCATC	TGCCCGCGCT	GTTGCTGCAC
151	TCGGCGCACT	AGTCGCGCGG	GGACGATGGA	ATAAGCCAAG	ATGCCGTTTT
201	CGTGGATGTT	TTCCGCAGGG	TGAAAGATTT	GCACGTTGTC	ATTGTTCAAA
251	CGGCATACGA	TTACGGAAAT	TTCACTGCGC	AAATCCACCA	TTTTTTCCAA
301	AACGCAATCC	ACGCCGCCGT	GTTCCGCAAA	CGCGGCTTTG	AGTTCATCCA
351	ATGTTTTTAC	GCGGATTTGA	CTTTGCCCGT	CGTAGCCCAA	CGTAGCCGTT
401	TTCAGGATGC	CGGGCAAAA	TTGCGCGCCT	GCTTCAGTGA	TGTCTTCAGC
451	CTTACAACAC	ACTTGATACG	GCGCGGTTTG	CAATCCCGCT	TGCGGTATCC
501	ATGCCCTTTC	CTGAATGCGG	TTTTGTGCAA	TGCCCAACA	ATCCGCGCTA
551	GGGGAACAT	TGGTATGTTT	TGCCAAAAAG	CGCATCGCAT	CGGCATTGAC
601	GTTTTCAAAT	TCAGTGGTCA	CGGCCGCGCA	TTTTGCCAAT	TCGTCCAAAG
651	CAGCTTTGGT	GTTAAACCGC	GCGCACAAT	GGCGGTCGGC	AAATTCTGCT
701	GCCGGCGCGT	CCGGATCGGG	GTCGAGAACG	GTTACTTTGT	AGCCCCATGT
751	TTTGGCGGCA	ACGGTAAACA	TTCTGCCTAA		

m658 . pep

1	MVSGIVRARG	DFVDDQFMRV	TDNKHFYRQY	ADIIQFVRQA	LRHLPRLLLLH
51	VGTHAAQVDDG	ISQDAVFVDV	FGRVSLHLVV	ISQTAYDYGK	FTAQIHHFFQ
101	NATHAASFGDG	RGEFELQCFY	ADLTFAVVAQ	RVRFQDAGQK	LRACFSDFVS
151	LTNHLIRRLG	QSREAYPCLF	LNAVLCNRHT	IAARGNIGMF	CQKAHRIGID
201	VKFSGHRRRA	FCQFVQSSLV	VKRRQAQMAVG	KFCCRRVRIG	VENGYFVAHG
251	FGGNGKXSA*				

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

BNSDOCID: <WO__8957280A2 | >

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:|||||:|||||
IENGYFVAHGFSNGKHSAX
      250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>>:

a658.seq

1	ATGGTGGCCG	GAATTGTGCG	GACGCGGCGC	GATTTCGTTG	ACGACCAATT
51	CATGCGTGTC	GCCGACAACA	AACATTTCTA	CCGCCAATAC	GCCGACGTAG
101	TTCAATTCAT	CGGCCAAACG	CTGCGCCATT	TGTCGCGCCT	GTTGCTGAAT
151	GTCGGCACTC	AGTCGGGCTG	GGACGATGGA	GTAGGCGGAG	ATACCGTTTT
201	CGTGAATGTT	TTCCGCAAGG	TCGAAAGTTT	GCACGTTGTC	ATTGTTCCAA
251	CGGCATACGA	TAACGGAAAT	TTCGCGCGCG	AAGTCCACCA	TTTTTTCCAG
301	AACGCAATCC	ACGCCGCGGT	GTTGCGCAAA	CGCGGCTTTG	AGTTTCATCCA
351	CCGTTTTGAC	GCGGATTTGG	CCTTTGCCGT	CATAGCCCAA	TGTAGCGGTT
401	TTCAGGATGC	CGGGCAGAAA	TTGTATGCTT	TCTTTCAGTA	TGTCTTCGGC
451	TTTGCAAATT	GCTTGATACG	GCGCGTTTGG	CAGGCCGTGT	TTGCGTATCC
501	ATGCCTTTTC	CTGAATGCGG	TTTTGCGCGA	TGGCAACGCA	TTCGCGCTGC
551	GGGGAAACAT	TGTTATGTTT	GGCGAGAAAA	CGCATCGCAT	CGGCATTGAC
601	GTTTTCGAAC	TCGGTCGTAA	CAGCCGCACA	TTTTTGCCAAT	TCTTCCAAAG
651	CGGTTTGSTT	GTCAAACGGC	GCACACAAAT	GGCGGTCGGC	AAATTCCGCT
701	GCCGGCGCAT	TCGGGTTGGG	ATCGAGTACG	GTTACTTTGT	AGCCCATGGT
751	TTTGGCAGCA	ACAGTAAACA	TTCTGCCTAA		

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep

1	MVAGIVRTRR	DFVDDQFMRV	ADNKHFYRQY	ADVVOFIGQT	LRHLSRLLLN
51	VGTSQGWDDG	VGEDT <u>VFVNV</u>	FGRIESLHVY	IVQTAYDNGN	FAAQVHHFFQ
101	NAIHAAVFGK	RGFEFTHRED	ADLAFAVIAQ	CSGFQDAGQK	LYAFFSDVFG
151	FANCLIRRLG	QACFAYPCLF	LNAVLRDNGA	VAAGNGIMGF	GKETHRIGID
201	VFELGRNSRT	FCQFFQSGLV	VKRRTQMAVG	KFRCRRIRVG	IEYGYFVAHG
251	FGSNSKHSA*				

m658/a658 75.3% identity in 259 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
 151 ACCGGAAAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
 201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
 301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
 351 CGAGccgctg gttgcCgcca tTtggaggc ggtggtcAAG GCGGCGGcg
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
 451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
 501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgCGTTAC
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
 601 CGGCGACATC actTCgccgc AAAAAGCCGC CGccgTCCTC AAACAAACCG
 651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
 701 TTCCGCGATT TGAAGCATTA TGCCGAACAC GGCCTTTTAC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
 801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGGCGAAAT GCGCGACGGC GAACAGGCGC GCGCTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
 201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
 251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTTGAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq
 1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
 151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
 351 CGAGCCGCTG GTTGCCGCCA TTTTGGAAAG CGTCGTCCGT GCGGCAGGCG
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
 451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
 501 CGTCC.AC GG ACGCAGCGGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
 551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
 601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
 701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTC GCCTGCCTT
 751 GAGTTTGGCA GAATGCGCG CCGCTATTTT GAACCACATC CGCGCCATAC
 801 ACGCGTTTTA CGGCGACACC GCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGACGAAAT GCGGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHDDQN
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPFETL CRTRCFAACL
 251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVSLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSHPGLGQRRHFAAKSRRRPQTNRRRRHDRARRARQAVVLPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

a661.seq	1	ATGCACATCG	GCGGCTATTT	TATCGACAAC	CCCATCGCAC	TTGCGCCGAT
	51	GGCGGGCATT	ACCGACAAAC	CGTCCGCCG	ACTTGCCGA	GATTTTGGCG
	101	CAGGTTGGGC	GGTGTGCGAA	ATGCTGACCA	GCGACCCGAC	GCTCAGAAAT
	151	ACTAGAAAAA	CCTTGCACCG	CAGCGATTTT	GCCGATGAAG	GCGGCATTGT
	201	TGCCGTGCAG	ATTGCCGGAA	GCGATCCGCA	GCAGATGGCG	GATGCCGCGC
	251	GTTACAACGT	CAGCCTTGGG	GCGCAGCTTA	TCGACATCAA	CATGGGCTGT
	301	CCCGCTAAAA	AAGTCTGCAA	TGTCCAAGCC	GGTAGCGCGC	TGATGCAGAA
	351	CGAGCCGCTG	GTTGCCGCCA	TTTTGGAGGC	GGTGGTCAAA	GCGGCGGGCG
	401	TACCCGTTAC	CCTCAAAACC	CGTTTGGGTT	GGCACGACGA	CCATCAAAAC
	451	CTGCCCGTCA	TCGCCAAAAT	CGCCGAAGAT	TGCGGCATTG	CCGCCCTTGC
	501	CG.TCCACGG	ACGCACGCGC	ACGCAAATGT	ACAAAGGCGA	AGCGGCTTAC
	551	GACCTGATTG	CCGAAACCAA	ATGCCGTCTG	AACATCCCGG	TCTGGGTCAA
	601	CGGCGACATT	ACCTCGCCGC	AAAAAGCCCA	AGCCGTCTCT	AAACAAACCG
	651	CCGCAGACGG	CATTATGATA	GGGCGCGGCG	CGCAAGGCAG	ACCGTGGTTC
	701	TTCCGCGATT	TGAAACATTA	CGCCGAACAC	GGTGTTTTAC	CGCCTGCCTT
	751	GAGTTTGGCA	GAATGTACCG	CCACTATTTT	GAACCACATC	CGAGCCATGC
	801	ACGCGTTTTA	CGGCGACACC	GCCGGTGTGC	GCATCGCACG	CAAACACATA
	851	GGCTGGTACA	TCGACGAAAT	GCCCGACGGC	GAACAGACAC	GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

a661.pep	1	MHIGGYFIDN	PIALAPMAGI	TDKPFRRLLC	DFGAGWAVCE	MLTSDPTLRN
	51	TRKTLHRSDF	ADEGGIVAVQ	IAGSDPQOMA	DAARYNVSLG	AQLIDINMGC
	101	PAKKVCNVQA	GSALMQNEPL	VAAILEAVVK	AAGVPVTLKT	RLGWHDHQN
	151	LPVIAKIAED	CGIAALAXPR	THAHANVQRR	SGLRPDCRNQ	MPSEHPGLGQ
	201	RRHYLAAKSP	SRPQTNRRRR	HYDRARRARQ	TVVLPFRFETL	RRTRCFACLE
	251	EFGRMYRHYF	EPHPSHARVL	RRHRRCAHRT	QTHRLVHRRN	ARRRTDTS*

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					


```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60
           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180
           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRHYDRARRARQAVVLPREFETL
           |:|:|
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRNRRHYDRARRARQTVVLPREFETL
           190     200     210     220     230     240
           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCARHTQTHRLVHRRNARRRDTSTX
           |||||:|||||:|:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||
a661      RRTRCFCTACLEFGRMYRHYFEPHPSHARVLRHRRCARHTQTHRLVHRRNARRRDTSTX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCCGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTCG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTIQ FYPAWKSFFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

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201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTTCGAC GCAACGATTG GGTTTTTGTG
601 GATTTTTTCG GTATTTCAGAC GGCAACGATT ACCGGATTGA GCCGATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTGA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
  1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
 51 KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VELIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVVF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP	RRRIGEINLAKCFPEWDEEK				
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
g663	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYASAKCLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVVFDFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVTLH				
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNNSVVFDFFGIQTATITGLSRIAALANAKVIPAI	PVREADNTVTLO				
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSP	DFYX				
g663	250	260	270	280	290	
	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSP	DFYX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
  1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
 51 TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGCGGAAAT CAATTGGCA

```

a663.pep

1	MCIEMKFIFF	VLYVLQFLPF	ALLHLKADLT	GLLAYLLVKP	RRRIGEINLA
51	KCFPEWDGKK	RKTVLQHFHK	HMAKLMLLEY	LYWYAPAGRL	KSLVRYRNKH
101	LYDDALADGE	KVILLYPHFT	AFEMAYVALN	QDVELISMSY	HQKNKILDEQ
151	ILKGRNRYHN	VFLIGRTEGL	RALVKQFRKS	SAPPLYLPDQ	DFRGNSVVFV
201	DFKGIRTATI	TGLSRIRALA	NAKVIPIAIV	READNTVLTH	FYPWASEFSP
251	EDAQDAQRM	NRFEIEVRV	HPEQYFWLHK	RFKTRPEGSF	DFY*

m663/a663 96.2% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
a663	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
a663	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
a663	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
a663	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
a663	250	260	270	280	290	

g664.seq

1	ATGATACATC	CGCACCACCTT	CCGCGCCTTT	TTCATAAACG	GTCATGGTGT
51	AGAAATTGTT	CATCTCCTCA	TAGCTGAcgg	gGCGCACCGG	ATGGGCGGTC
101	GGGCTTCGCT	CTTCGGGGAA	CTGGTTCCTGG	CGCAGCAGGC	GGATGTTCTC
151	GATCGCGGCG	ACGCGCGCGG	CGGCGCGGCT	GCCGGAAAC	TCTTGGTCGC
201	GGAACACGGT	CAGCCCTTCC	TTCAGCGAAA	CTTGGAACCA	GTCGCCACGA
251	GTTACGCGGT	TGCCCCGTCCA	GTTGTGGAAA	TATTCGTGTC	CGCACCAGGA
301	TTCAATGCCT	TCGAAATCGG	TATCGGTGGC	GGTGC GGCTG	TCGGCGAGGA
351	CGAACTTGGT	GTTAAAAATG	TTCAAACCCCT	TGTTTTCCAT	CGCGCCCAT
401	TTGAAATCGC	CTACGCGGAC	GACCATGAaa	atatccaagt	cataTTCcaa
451	cCgaagcgc	gtttcgteCc	acttcatacgC	gtTTTTTCAA	cgaTTCACG
501	GCAAAGCCGA	CCTTGGGTTT	GTCCGCTTCG	GTGGTGTAAA	ACTCAGATTTT

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGGRACVFGE  LVLAQQADVL
51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101 FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151 PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GCGGCACCGG  ATGGGCGGTC
101 GGGCCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTT
151 GATGCGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTTCG
201 GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAACCA  GTCGCGGCAG
251 GTTACGCGGT  TGCCCGTCCA  GTTGTGGAAA  TACTCGTGTC  CGACCACGGA
301 TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351 CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTTTTCCAT  CGCGCCCAT
401 TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451 ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTT.CAA  CGATTCCACG
501 GCAAAGCCGA  CCTTGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGGRACVFGE  LVLAQQADV
51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101 FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFF
151 TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGGRACVFGE	LVLAQQADV	FDAHGAAGAV
	:	:	:	:	:	:
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGGRACVFGE	LVLAQQADV	LDAHGAAGAV
	:	:	:	:	:	:
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	GAAVGKDELG
	:	:	:	:	:	:
g664	AGKLLVAEHG	QPFLQRKLEP	VAAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	GAAVGEDELG
	:	:	:	:	:	:
	130	140	150	160	170	180
m664.pep	VKDVQTLVFH	RAHIEIAHGD	DHENIQVVFF	QTEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
	:	:	:	:	:	:
g664	VKNVQTLVFH	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	:	:	:	:	:	:
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC  CGCACCCTT  CCGCGCCTTT  TTCATAACG  GTCATGGTGT
51  AGAAATTGTT  CATCTCCTCA  TATCGGGCGG  GCGGCACCGG  ATGTGCGGTC
101 GGACCTGCGT  CTTGCGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTT
151 GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTTCG

```

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF  FINGHGVEIV  HLLISGGAHR  MGRTCVFGE  LVLAQQADV
51  DTAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGHAVARP  VVEIFVSDHG
101 FDAFKIGIGG  GTAVGKDELG  VKDVQTLVFH  RTHIEIAHGD  DHENIQVVFQ
151 TEARFVPLHC  VFXAIPRQSR  PWACPLRWCK  TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGEVLVAQQADVFDAAHGAAGAV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         VIHPHHFRAFFINGHGVEIVHLLISGGAHRMGRTCVFGEVLVAQQADVFDTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664.pep    AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDFAEIGIGGGAAGVKDELG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDFAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPQRSRPWACPLRWCK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a664         VKDVQTLVFHRTTHIEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPQRSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              | | |
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG  acgaaacgcg  cttcgGgttg  GAAtatgact  tggatatttT
51  CATGGTCGTC  GCGTAGGCG  ATTTCAATAT  GGGCGCGATG  GAAAACAAGG
101 GTTTGAACAT  TTTTAACACC  AAGTTCGTCC  TCGCCGACAG  CCGCACCGCC
151 ACCGATACCG  ATTTCGAAGG  CATTGAATCC  GTGGTCGGAC  ACGAATATTT
201 CCACAACTGG  ACGGGCAACC  GCGTAACCTG  CCGCGACTGG  TTCCAGCTTT
251 CGCTGAAGGA  AGGGCTGACC  GTGTTCCGCG  ACCAAGAGTT  TTCCGGCGAC
301 CGCGCCGCC  GCGCCGTGCG  CCGCATCGAG  AACATCCGCC  TGCTGCCCCA
351 GAACCACTTC  CCCGAAGACG  CAGGCCCGAC  CGCCCATCCG  GTGCGCcccg
401 TCAGCTATGA  GGAGATGAAC  AATTTCTACA  CCATGACCGT  TTATGAAAAA
451 GGCGCCGAAG  TGGTGCGGAT  GTATCATACC  CTGCTCGGCG  AAGAGGGCTT
501 CCAAAAAGGC  ATGAAGCTAT  ATTTcCaacg  CCACGACGGA  CAGGCAGTGA
551 CCTGCGACGA  TTTCCGCGCG  GCGatggcgg  ATGCGAACGG  CATCAATCTC
601 GACCACTTCG  CCTTGTGGTA  CAGCCAGGCG  GGCACGCCCG  TTTTGAAGC
651 CGAAGGCCGT  CTGAAAAACA  ATGTTTTCGA  GTTAACCATT  AAACAAACCG
701 TGCCGCCAC  GCCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCCGTC
751 AAAGTCGGGC  TTCTGAACCG  CAACGGCGAA  GCGGTGGCAT  TCGATTATCA
801 GGGCAAACGC  GCAACCGAAG  CCGTGTGTGCT  GATGACCGAA  GCCGAACagg
851 CCTTCCCGCT  CGAAGGTGTA  ACCGAAGCCG  TCGTTCCCTC  GCTGCTGCGC
901 GGGTTCAGCG  CGCCAGTGTA  TCTGAACAT  CCGTACAGCG  ACGACGACCT
951 GCTGCTCCTG  CTCGCCACG  ACAGCGACGC  TTTCACGTGC  TGGGAAGCCG

```

```

1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTTcgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcAA gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTTATCGGCT CAAGccggcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
1 MKWDETRFGL EYDLDFIMVV AVGDFNMGM ENKGLNIFNT KEVLADSRTA
51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VREVSYEEMN NFYTMTVYEK
151 GAENVVMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPTPDM ADKQPMPIPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAVPVLYN PYSDDDLLLL LAHSDAFTC WEAQOTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTCCGCG ACCAAGAATT TTCCGCGGAC
301 CGCGCCAGCC GCGCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAATTG CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGC GCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAATTG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCCCGATATG ACGGATAAAC AGCCGATGAT GATCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGC AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

```

```

1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTGCGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPPTPDM TDKQPMPIPV
251 KVGLLNRRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQAOTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQQA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLNPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

```

m665.pep      10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES
g665           10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES

m665.pep      70      80      90     100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHOF
g665           70      80      90     100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRR IENIRLLRQHOF

m665.pep     130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
g665          130     140     150     160     170     180
PEDAGPTAHPVRPVSYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG

m665.pep     190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM
g665          190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPTPDM

m665.pep     250     260     270     280     290     300
TDKQPMPIPVKVGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR
g665          250     260     270     280     290     300
ADKQPMPIPVKVGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR

```

m665.pep	310	320	330	340	350	360
	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTWRWEAAQTLYRRVAANLATLSDGVELPKHEK					
g665	: : : : : :					
	310	320	330	340	350	360
	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRVAANLAALSDGIGLPKHEK					
m665.pep	370	380	390	400	410	420
	LLAAVEKVISDDLLDNAFKALLLGVPSEAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	: : : : : :					
	370	380	390	400	410	420
	LLAAVEKVISDDLLDNAFKALLLGVPSEAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
m665.pep	430	440	450	460	470	480
	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	: : : : : :					
	430	440	450	460	470	480
	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
m665.pep	490	500	510	520	530	540
	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
g665	: : : : : :					
	490	500	510	520	530	540
	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
m665.pep	550	560	570	580	590	600
	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	: : : : : :					
	550	560	570	580	590	600
	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
m665.pep	610	620	630	639		
	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	: : : : : :					
	610	620	630			
	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

a665.seq

1	ATGAAGTGGG	ACGAAACGCG	CTTCGGTTTG	GAATACGACT	TGGATATTTT
51	CATGGTCGTC	GCCGTGGGCG	ATTTCAATAT	GGGTGCGATG	GAAAACAAGG
101	GTTTGAACAT	CTTTAACACC	AAGTTCGTCC	TTGCCGACAG	CCGTACCGCC
151	ACCGATACCG	ATTTTGAAGG	CATCGAATCC	GTGGTCGGAC	ACGAATATTT
201	CCACAACCTGG	ACGGGCAACC	GCGTGACCTG	CCGCGACTGG	TTCCAGCTTT
251	CGCTGAAGGA	AGGGTTGACC	GTGTTCCGCG	ACCAAGAATT	TTCCGGCGAC
301	CGCGCCAGCC	GCGCCGTGCG	CCGTATCGAA	AACATCCGCC	TGCTGCGCCA
351	GCACCACTTC	CCCGAAGACG	CAGGTCCGAC	CGCACATCCG	GTGCGCCCCG
401	CCCGATATGA	GGAGATGAAC	AATTTCTACA	CCATGACCGT	TTATGAAAAA
451	GGCGCGGAAG	TGGTGCGGAT	GTATCACACC	TTGCTCGGCG	AAGAGGGCTT
501	CCAAAAAGGT	ATGAAGCTCT	ATTTCCAACG	CCACGACGGA	CAGGCTGTTA
551	CCTGCGACGA	TTTCCGCGCG	GCGATGGTGG	ACGCGAACGG	CATCAACCTC
601	GACCAATTCG	CCTTGTGGTA	CAGCCAAGCA	GGTACGCCGG	TTTGTAGATG
651	TCAAGGGCGT	CTGAAAAACA	ATGTGTTTGA	GTTAACCATC	AAACAAACCG
701	TGCCGCCAC	GCCCGATATG	GCGGACAAAC	AGCCGATGAT	GATTCCTGTC
751	AAAATCGGGC	TGCTGAACTG	CAACGGCGAA	GCGGTGGCAT	TTGATTATCA
801	GGGCAAACGC	GCGACCGAAG	CCGTGTTGCT	GCTGACCGAA	GCCGAACAGA
851	CCTTCCAGTT	CGAAAGCGTA	ACCGAAGCCG	TCGTTCCCTC	GCTGCTGCGC
901	GGGTTACAGC	CGCCGGTGCA	TCTGAACTAT	CCGTACAGCG	ACGACGACCT
951	GCTGCTTCTG	CTCGCCCATG	ACAGCGACGC	CTTCACGCGC	TGGGAAGCCG
1001	CACAAACGCT	CTACCGCCGT	GCCGTCGCCG	CCAACCTTGC	CGCGCTTTCA
1051	GACGGCGTCG	AGTTGCCGAA	ACACGAAAAA	CTGCTTGCCG	CCGTGAAAAA
1101	AGTCATTTCA	GACGACCTCT	TAGACAACGC	TTTCAAAGCC	CTGCTTTTGG
1151	GTGTGCCGTC	TGAAGCCGAG	CTGTGGGACG	GCGCGGAAAA	CATCGACCCG
1201	CTGCGCTACC	ATCAGGCGCG	CGAAGCCTTG	TTGGATATAC	TTGCCGTCCG
1251	CTTTCTGCCG	AAATGGCAGC	AATTGAACCG	TCAGGCGGCG	AAGCAGGAAA
1301	ACCAAAGCTA	CGAGTACAGC	CCCGAAGCCG	CCGTTGGGCG	CACGCTGCGC
1351	AATGTCTGCC	GCGCCTTCGT	CCTGCGCGCC	GATCCCGCGC	ACATCGAAAC

a665.ppt

1	MKWDETRFGL	EYDLIDFMVV	AVGDFNMGAM	ENKGLNIFNT	KEVLADSRTA
51	TDTDFEGIES	VVGHEYFHNW	TGNRVTCRDW	FQLSLKEGLT	VFRDQEFSGD
101	RASRAVRRIE	NIRLLRQHOF	PEDAGPTAHP	VRPARYEEMN	NEYTMTVYEK
151	GAEVVRMYHT	LLGEEGFQKG	MKLYFORHDD	QAVTCDDFRA	AMVDANGINL
201	DQFALWYSQA	GTPVLDAQGR	LKNNVFELTI	KQTVPTPDM	ADKQPMPIPV
251	KIGLLNCNGE	AVAFDYQGKR	ATEAVLLLTE	AEQTFQFESV	TEAVVPSLLR
301	GFSAPVHLNY	PSYDDDLLLL	LAHDSDAFTR	WEAAQTLYRR	AVAANLAALS
351	DGVLEPKHEK	LLAAVEKVIS	DDLLDNAFKA	LLLQVPSEAE	LWDGAENIDP
401	LRVHQAREAL	LDILAVRFLP	KWHELNROQA	KQENQSYEYS	PEAGGWRTLR
451	NVCRAFLVRA	DPAHIETVAE	KYAEMAQNMT	HEWGILSAVN	GNESDTRNRL
501	LAQFAKDFSD	DALVMDKYFA	LVGSSRRSDT	LQQVQTLQHC	PKFSLENPNK
551	ARSLIGSFSR	NVPHFHAEDG	SGYRFIADKV	EIEDRFNPQV	AARLVQAFNL
601	CNKLEPHRKN	LVKQALQRIR	AQEGLSKDVG	EIVGKILD*	

m665/a665 97.3% identity in 638 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGLEYDL	IFMVVAVGDFNMGAMENKGLN	IFNTKFVLADSRTATD	TDFEGIES		
a665	MKWDETRFGLEYDL	IFMVVAVGDFNMGAMENKGLN	IFNTKFVLADSRTATD	TDFEGIES		
	10	20	30	40	50	60
m665.pep	VVGHEYFHNW	TGNRVTCRDWFQ	LSLKEGLTVFRDQ	EFSGDRASRAVRRIENIR	LLRQHQF	
a665	VVGHEYFHNW	TGNRVTCRDWFQ	LSLKEGLTVFRDQ	EFSGDRASRAVRRIENIR	LLRQHQF	
	70	80	90	100	110	120
m665.pep	PEDAGPTAHPVR	PASYEEMNNFYTM	TVYEKGAEVVRMYHTLL	GEEGFQKGMKLYFQR	HDG	
a665	PEDAGPTAHPVR	PARYEEMNNFYTM	TVYEKGAEVVRMYHTLL	GEEGFQKGMKLYFQR	HDG	
	130	140	150	160	170	180
m665.pep	QAVTCDDFRAAM	ADANGINLDQFALWYSQ	AGTPVLEAEGRLKNNIFEL	TVKQTVPTPDM		
a665	QAVTCDDFRAAM	VDANGINLDQFALWYSQ	AGTPVLDAQGRKNNVFEL	TIKQTVPTPDM		
	190	200	210	220	230	240
m665.pep	TDKQPMMPVKVGL	LLNRNGEAVAFDYQG	KRATEAVLLLTEAEQTF	LLEGVTEAVVPSLLR		
a665	ADKQPMMPVKIG	LLNCNGEAVAFDYQG	KRATEAVLLLTEAEQTF	QFESVTEAVVPSLLR		
	250	260	270	280	290	300
m665.pep	GFSAPVHLNYP	PSDDDLLL	LAHDSDAFTRWEAAQ	TLRYRAVANLAT	SDGVELPKHEK	
a665	GFSAPVHLNYP	PSDDDLLL	LAHDSDAFTRWEAAQ	TLRYRAVANLAAL	SDGVELPKHEK	
	310	320	330	340	350	360

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLDDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLDDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILD					
a665	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1   ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATCTTTGAA ACCGAACTGC ATTTGACAT  TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAACT  CTTGTCCGTC AAAATCAACG GCGCGGGCGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG  CTATCCCGTT
451 TTGCTTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC  ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTC CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CCACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCCGC
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TCGCCAGAA  CCACTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAGGC  GCGGAAGTGG
1151 TCGGGATGTA TATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGC  ACGCCCGTTT TGAAGCCGA  AGGCCGCTG
1351 AAAACAATG  TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA  GTCGGGCTTC
1451 TGAACGCCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACCGCGA
1501 ACCGAAGCCG TGTGCTGAT  GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA  GCGACGCTT CACGTGCTGG GAAGCCGCC  AAACGCTCTA
1701 CCGTCGCGCC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAAATCT CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACCTG TGGGACGGCA CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTGT GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGGAAG CAGGAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGCGC CGACACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLIDFMVVA
251 VGDFNMGAME NKLNI FNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVVRRIEN IRLLRQNFPP
351 EDAGPTAHVP RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDFFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK VGLLRNNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAKAL LLGVPSEAE WDGTEIDPL RYHQAREALL DTLAVRFLPK
651 WHELDRAAK QENQSYEYSP ETADWRTRLN VCRAFLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QVQVTAQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFTADKVI EIDRFNPQVA ARLVQAENLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCCG
101 TGAAGTCGCG TTTGACGGT GAGCCGAGA GGGTAGGGGA GCCGCTGGTG
151 TTGACGGTT CGGCGAACT CTTGTCCGTC AAAATCAACG GGGCGCGGCG
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGCGCGC AATTGTGTTT CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC ACAAAAAACG CTATCCCGTT
451 TTGCTTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTT CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTTC CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGCAGCG CATCGAAAAC ATCCGCTGCG TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCTTG CTGCGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCCGTTT TGGAAGCGGA AGGTCTGCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGCTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ACTATCAGGG CAAACCGCGC

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCGGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCGCGCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGGCGCGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCCTG CAACAGGTTG GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCAACG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGCAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDDRHWV KWEDPFSSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPPTPDMT DKQPMMPVK VGLLRNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFLEGV T EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVID
601 DLLDNAFKAL LLGVSEAE LWDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVG E IVGKILD*

m665-1/g665-1 96.1% identity in 866 aa overlap

m665-1.pep	10	20	30	40	50	60
	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRILE	TELHFDIAEP	QTVVKSRLTV	EPQRVAGEPLV	LDGSAKLLSV
	10	20	30	40	50	60
m665-1.pep	70	80	90	100	110	120
	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	70	80	90	100	110	120
m665-1.pep	130	140	150	160	170	180
	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDDRHWV	KWEDPFSSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDDRHWV	KWEDPFSSKPS
	130	140	150	160	170	180
m665-1.pep	190	200	210	220	230	240
	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTEDRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	190	200	210	220	230	240
m665-1.pep	250	260	270	280	290	300
	YDLDFMVVAV	GDENMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGEYFHNWT
g665-1	YDLDFMVVAV	GDENMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGEYFHNWT

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHOFEPEDAGPTAHPV					
g665-1	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRRIENIRLLRQHOFEPEDAGPTAHPV					
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNMFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORHDGQAVTCDDFRAA					
g665-1	370	380	390	400	410	420
	RPVSYEEMNMFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORHDGQAVTCDDFRAA					
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDMDKQPMIIPVK					
g665-1	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPTPDMADKQPMIIPVK					
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLHDSDAFTRWEAAQOTLYRRAVAANLATLSDGVLPKHEKLLAAVEKVISD					
g665-1	550	560	570	580	590	600
	YSDDDLLLHDSDAFTCWEAAQOTLYRRAVAANLAALSDGIGLPKHEKLLAAVEKVISD					
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	670	680	690	700	710	720
	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA					
g665-1	730	740	750	760	770	780
	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	790	800	810	820	830	840
	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILDX					
g665-1	850	860				
	VKQELQCIRAQEGLSKDVGEIVGKILGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTGATAT TAACGAACCG CAAACCATG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAACAAAC CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

```

```

501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGGTCG GGGCGATTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCCTGC TCGCGCAGCA CCAGTTCCCC
1051 GAAGACGCGAG GTCCGACCGC ACATCCGGTG CGCCCCGCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGACAG GCTGTACCT GCGACGATTT
1251 CCGCGCGCGG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGTTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTCGAGTT AACCATCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTCAA CGGCGAAGCG GTGGCATTG ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCAATC GAACATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCATGACA GCGACGCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGTGCCG GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCGCTCTGA
1851 AGCCGAGCTG TGGGACGCGC CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCAC GAATGGGGCA TCCTGTCCCG
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTTC
2251 GTCGGCTCAA GCCGCCGCG CAGACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHOF
351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEFGQKGM
401 KLYFORHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAGGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIPVK IGLLNCNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAK QENQSYEYSP EAAGWRTLRLN VCRAFLVLRAD PAHIETVAEK
701 YAEMAQNMTM EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QVQTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRRA
851 QEGLSKDVG EIVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV LDGSAKLLSV					
m665-1	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGPELV LDGSAKLLSV					
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGGRNVKIEFYTTTEADKPKVGF AVESLKNAMKWDETRFGL
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLADSRATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTPPTPDMA DKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQ GKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQTLYRR AAVANLAALSDGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLLGV PSEAE LWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQA AK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTL RNVCFVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSD DALVMDK YFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

```

          790      800      810      820      830      840
          850      860
a665-1.pep  VKQALQRIHQEGLSKDVGEIVGKILDX
             |||||
m665-1      VKQALQRIHQEGLSKDVGEIVGKILDX
             850      860

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGAAGGAG TGCTTGTAGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CCGCACCGAT GCGTGCACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGTAGGTAC GCCTGCTATC CCTAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GCGAAGGAG TGCTTGTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CCGCACCGAT GCGTGCACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

```

          10      20      30      40      50      60
m666.pep  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          | |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g666       MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTHSAVIAGADAHTPE
          10      20      30      40      50      60
          70      80      90     100     110     120
m666.pep  HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSAAADAMVAVQTTL SLVEPQSSGL

```



```
a666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CAGCGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAAGCAG GTGATTGCAA GTGATTTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CCGCACCGAT GCGTGGCAGC
451 CCGGAATTAT TTTTGATATA AGATGGTCAA CCATTGAAAT TGTGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

```

a666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCOVIHAN QGKVNTHSVA
51 ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLWDYD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFEAVVV VARWRLLSL N*

```

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHTSA	VITGADAHTPE
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHTSA	VITGADAHTPE
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAMV	AVQTTLTSLV	EPQSSGL
a666		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAMV	AVQTTLTSLV	EPQSSGL
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWD	NTAKTLTTFD	GRE	TAPMRATPEL	FLDKDGQPL	KFMEAVVVVARWVRLLSL
a666		GGGAFVLYWD	NTAKTLTTFD	GRE	TAPMRATPEL	FLDKDGQPL	KFMEAVVVVARWVRLLSL
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgctcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCAAttg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATAACG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CCGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCgcCT
801 ATTgTgtcat TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1  MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGA V MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRL LCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1  ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCGGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVYQGA V MQYGQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10          20          30          40          50          60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          | | : : | | : : | | : : | | : : | | : : | | : : | | : :

```

a667.seq

1	ATGCGGTTTG	TCTTCTGTTT	GGGCGGAGAG	ATAGTTTCTG	ATCCGCTTGA
51	TTTCCATTTC	GTATTCTGCT	GCGTCGAATC	TGCCGCTGAC	CAGACAGAAA
101	CCGAGATACA	TCAGATAGGT	ATTTACCGCA	TCGGTTTCGG	AATAATTTCG
151	GATTTCCTTC	AGCCTGCCCC	CGTGGAAACG	CTCCACACC	TTGCTGCCCT
201	CCATACCCAG	CTTGCCCGGA	AAACCGCACA	GTTTCGCCAT	ATCGTCCAAC
251	GGCAGATTGC	CCCTCGGCTG	GTAAGCGCG	AGCAAATCCA	TCAAATCGCA
301	ATGACGTTGG	TGGTAGCGCG	TGATGTAGTT	GTTCCACTTG	AAATCGCGGC
351	TGTCGCCGAA	ATCGCCGTCG	CCCATCTCCC	AATAGCGCGC	GGCGTTGATG
401	CCGTGTAGCA	GCGAACGGTA	ATGCAGAAC	GGCAGGTGCA	AACCGCCGCC
451	GTTCCAACTG	ACCAGTTGCG	GCGTATGTTT	TTCAATCAAC	TCGAAAAATT
501	TGGCGATAAC	CACTTCTCTG	CCGTCAATCA	TCTCGCCGAT	TGTACCGACA
551	TGGACTTTAT	CCTGCCCTCA	ACGCATGCAG	CACGAAATCG	CCACAATCTG
601	ATGAAGATGA	TGCTGCATAA	AATCCCACCC	CGTCTGAGCA	CGGCGTTTTT
651	GCTGGGCAAA	CAGCACCCT	TCATCGTCGG	GCAGCGAGGA	CGGCAAGTCA
701	TACAGCGTAC	GGATACACTG	CACATCGGGT	ACGGTTTCAA	TATCGAAAGC
751	CAAAATCGTG	GTCATGACAG	CACCTTGAT	TTAAAA.CAG	ACTTGCGCCT
801	ATTGTGTCAT	TAA			

a667.pep

1	MRFVFC LGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVGRHIRPRL	VKREQIHQIA
101	MTLVVAADV	VPLEIAVAE	IAVAHIPIAR	IGVDV*QRTV	MNQROVETA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHN
201	MKMMHLKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRTDTL	HIGYGFNIES
251	QNRGHDSTLY	LKXDLRLLC	*		

```
m667.pep      10          20          30          40          50          60
               MRLLFPGLCGQVIPHFPDFHFVFVRIQPAADQTETQVHQISVCRVGFALLIADFLQPARMEE
a667           ||: | |: :: |:||||| : : |||||:::||: |:|||||:|||||:
               MRFVFCLGGEIVSDPLDFHFVFCVESAAADQTETQIHQIGIYRIGFAIIADFLQPARVER
               10          20          30          40          50          60

               70          80          90          100         110         120
m667.pep      LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAVAE
               ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a667           LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAADVVPLEIAAVAL
```

	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	IAVAHIPIARGVD	AVYQGAVM	QYGGIETA	AAVPTD	QLRRMFFN	QFEKFSNDHFLAVIHLAD
a667						
	130	140	150	160	170	180
m667.pep	190	200	210	220		
	GADMYFILP	PTHAARNR	HNLMMK	MLHKKIA	ARLSTAF	VLGNQHHL
a667	:					
	190	200	210	220	230	240
a667	CTDMDFILP	PTHAARNR	HNLMMK	MLHKIPT	RLSTAF	LLGKQHHFIVGQRGRQVIQRTDTL
	190	200	210	220	230	240
a667	HIGYGFN	IESQNR	RGHDST	LYLKX	DLRLL	CHX
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

g669.seq

1	ATGCGCCGCA	TCGTTAAAAA	ACACCAGCCC	GTAAACGCGC	CACATATCGT
51	TTTGGAAATT	CGGATAATGA	AACTGCATCG	CGCGTTTGTC	TTCCTTTGGGC
101	GGAAACGTC	CATCATCAT	GACCGCAGCC	TTCGGCGTCA	ACACGGGATC
151	GAAGGATGG	GTTTCGATTT	CAAGCAGATT	TTCAGACACG	TTCAATCCTC
201	CAACAGGCA	AGCGGCAGAC	AGCCGGTTTG	CACCAAACCG	CCAAACACGG
251	CAAGCCTTA	AACAGCATTA	TCACGCCCTG	CCGTTTTTCG	TTACAATGCC
301	GACATCAAAC	GGATACGTGA	A		

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

g669.pap
1 MRRIVKKHQP VNAPHIVLEI RIMKLRHAFV FLGRKRPHHH DRSLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101 DIKRIL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```
m669.seq
1  ATGCGCCGCA  TCATTAAAAA  ACACCAGCCC  ATAAACGCGC  CACATATCGT
51  TTTGGAAATT  CGGATAATGA  AACTGCATCG  CGCGCTTTGTC  TTCCTTTGGGC
101 GGAACGCTCC  CCATCATCAT  GACAGCAGCG  TTCGGCGGCA  ACACGGGATC
151 GAAGGGATGG  GTTTCGATTT  CAAGCAGATT  TTCAGACACG  TTCAATCCTC
201 CAACAGGCAA  AACGGCAGAC  AGCCGGTTTG  CACCAAACCG  CCAAACACGG
251 CAAGCCTTCA  AACAGCATT  TCACGCCCTG  CCGTTTTTCG  TTACAATGCC
301 GACATCAAAC  GGATACTGTA  A
```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```
m669.pep
  1  MRRIKKHQP INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101  DIKRIL*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

```

      10      20      30      40      50      60
m669.pep  MRRIKKKHQPINAPHIVLEIRIMKLHRAVFVFLGRKRPHHDSLSLRQHGIEGMGFDKQI
          |||:||||:|||||||||||||||||||||||||||||||||||||
g669      MRRIKKKHQPVNAPHIVLEIRIMKLHRAVFVFLGRKRPHHDSLSLRQHGIEGMGFDKQI
          10      20      30      40      50      60
          70      80      90     100

```

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
  1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
 51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101  GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151  GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201  CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251  CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301  GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
  1  MRRIKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLQTAL SRPAVFGYNA
101  DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
  1  ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
 51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTACGCAC
151  ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251  CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTC GCATTTTGCC
401  CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTRC
151  G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
  1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTAAA
 51  AAACGCTTTC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTACGCAC
151  ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACAAACATTA

```

```

251 CCGCGCGGTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
 151 G*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAK PRAIATRCCWPPESWEGKASFLCASPTRSK
              |||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||
g670           SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
  51 AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
 101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
 151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
 201 GCCGACCAT TCGGGGTGCA GTGCGGAGGT CGGTTTCGTC AACACATTA
 251 CCGCGCGGTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
 301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
 351 GCGTTCCAAA AGTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
 401 CTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
 451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
 151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
a670         FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
              |||||
a670         SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCGAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCAAA
201 GGCGAGGTcG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
              |||||
g671         MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```

a671.seq	1	51	101	151	201	251	301	351	401
	ATGACCAGCA	GGGTAATAAT	CAAAATGCCT	TTCAATGCAC	CGAATACGCC				
	GCCCCAAATG	CGGTGTGGCA	AGCCCCAAACC	GACCGCCGAA	ACTGCCCOGG				
	TCAGCAGCGA	CGCGAGTATT	TTCTGGATCA	GACAGGCAAT	GACGAATAGG				
	GAAATGAACG	ACAGAGCCAA	TGCAAAACAGG	CGGGGTGGGA	ACGATGCAAA				
	GGCGATGTCG	GCGAAGGGTG	CGGCAAAGAG	TTTGGCGAAA	AAAAAGGCCAA				
	CCACCCATGC	CGCCATTGAG	CCAGCCTTCG	CAATCACGCC	GCGCATCGCG				
	GATAGCACGA	TGCAGGCCGC	GATGATGGCG	GAGACAGGGA	GGTCGGCAAC				
	GGGGAGGTTA	TTCATTCCGT	ACCTGACCGG	CGATACCGTA	TACCGGCAAT				
	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTCGC	TTTTTATAGT	TGCTTGA				

```
a671.pap
1 MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51 EMNDRANANR RGWNDAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVEIVA*
```

```

      10      20      30      40      50      60
m671.pep  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
          |||||
a671      MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
          |||||

      70      80      90     100     110     120
m671.pep  RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL
          |||:| ||| |||||
a671      RGWNDAKAMSAKGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
          |||||

      130     140     149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          |||||
a671      FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          |||||

```

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCGACGGC	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCC	CCGCGCTATC	GACATCATT	AAGCACAATA	AATCGCCGCC
151	GCACTGCCGC	CGTTTGTCTAG	CGTTGTGCGC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCGGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CCGCCCTTAT
301	ATTAAGCCCA	TTCTGTGTTCA	GACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	GCGCTTCCCC	AACGCTCAGG	CAGTCTGTT	CGATGCCTAT	CACCTTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	Ggacgtgtgt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGCCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATC	CCGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRFN NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGCGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRFN DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQGSRAV	DIARAKKITA	ALPPFVSVVA
g672	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYPQSPRAI	DIIKAQKIAA	ALPPFVSVVA
m672.pep	70	80	90	100	110	120
	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRFN
g672	70	80	90	100	110	120
	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRFN
m672.pep	130	140	150	160	170	180
	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	130	140	150	160	170	180
	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
m672.pep	190	200	209			
	SGGVEASKGK	KDAKVAAFI	ATANRLSRX			
g672	190	200				
	SGGVEASKGK	KDKPAKVAAFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTGTC CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

              10      20      30      40      50      60
m672.pep      MRKIRTKICGITTTPEDAAAAAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA
a672           MRKIRTKICGITTTPEDALYA AHAGADALGLVFYQSPRAVDIKAQKITAALPPFVSVVA
              10      20      30      40      50      60

              70      80      90      100     110     120
m672.pep      LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
a672           LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
              70      80      90      100     110     120

              130     140     150     160     170     180
m672.pep      DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
a672           DAQALLFDAYHPSEYGGTGHFRFDWTLAEYSGKPWVLAGGLTPENVDEAIRITGAEAVDV
              130     140     150     160     170     180

              190     200     209
m672.pep      SGGVEASKGKKDAAKVAEFIATANRLSRX
a672           SGGVEASKGKKDPAKVAEFIATANRLSRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTAAG CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGCGG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTCCGT GAAAACTCT TCCGCTATTT

```

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
  1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
 51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCTGGGA GCGGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||||||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDH RNALNDRNLQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||||||

```

1080

```

g673      YTDDTAQFVFDTPGFQTDH RNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLF RYLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLF RYLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCGG ACGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCAGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTGAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 AREFLAMEIVR EKLF RYLGEEL LPYAMNVEVE QFEEEDGLNR
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVF LKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFGTDHRNALNDRNLNQNVTALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFGTDHRNALNDRNLNQNVTALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1   ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1   MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1   ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGAGACG AAGAATTGTT CAACAAACTT
151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1   MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLEFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLEFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAACAG	CCGCGCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCGCGGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep	1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
	51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
	101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*
m674/a674	99.3% identity in 141 aa overlap					
	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLEFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLEFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacggtc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEM	LKVCCRTLQELGVADENITVATVPGALEIP				
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAAGAA GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV

```


101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE	LSNESGAGVSRVALDYNIPIANAVLT	TEN			
a675	IALMNFASSEKFDALIAIGVVIRGETYHFE	LSNESGAGVSRVALDYNIPIANAVLT	TEN			
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLL	LEEQFEDEEX				
a675	DAQAIERIEEKASDAKVAVECANLVNLL	LEEQFEDEEX				
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTtg
51	ggAAACGGTG	CGCTTGCGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGGC	CTTCGGGCGT
151	GTTCAAACC	ACTTCGTGCG	CTTCGCGCGC	TTTAATCAGG	CAACGCGCCA
201	ACGGCGAAAT	CCAAGAAATT	TTGTTTTCG	CGGTATCGAT	TTCATCGACG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAATACTT	GGTCGGTTCG	TTTCGCGCAAT	TCGGGATCGA
351	CGACGACGGC	AGCCTCCAAA	CGTTTGGTCA	GGAAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGA	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTGAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep

1	MPQILVRIFL	IRYSFIWETV	RLCRFRRHSR	SVDFDVFDRK	DFNFLTAFRR
51	VQNHVFAR	FNQATRQRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT
101	GRAEKYLVR	FAQFGIDDDG	SLQTFGQETD	AAVDFAHTAF	AVKIVAVFAA
151	VAVACRPVDD	LDDFGAFFID	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGCTTTTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCGGGCGT
151	GTTCAAACC	ACTTCGTGCG	CTTCGCGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGTCGCGCA	ACAGTCCGAC
301	CGTCGCGCCG	AAAAACACTT	GGTCGGTTCG	TTTCGCGCAAT	TCGGGATCGA
351	CGACGACGGC	AGCCTCCAAA	CGTTTGGTCA	GGAAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGA	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTGTGAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep

1	MPQILVRIFL	IRYSFIWETA	RFCRFRHSR	SVDFDVFDRK	DFNFLTPFRR
---	------------	------------	-----------	------------	------------

51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSR	SVDFDVDRKDFNFLT	PFRRVQNHFAFAR			
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSR	SVDFDVDRKDFNFLTAFRRVQNHFAFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKYLVRFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCGCCA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAACC	ACTTCGTGCG	CTTCACGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGGTTCG	TCGCCGCAAT	TCGGGATCAA
351	CGACGACGGC	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVDRK	DFNLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQTD	
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVAVFAA	
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSR	SVDFDVDRKDFNFLT	PFRRVQNHFAFAR			
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSR	SVDFDVDRKDFNFLT	PFRRVXNHFAFTR			
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m677.pep      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
a677          FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDEGFAFFVDQLIKLVFQCL
a677          GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDEGFAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
a677          PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCGG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTt TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCCTcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTGCTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTt TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g678      MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ
          10      20      30      40      50      60

      70      80      90     100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||:|||||:|||||:|||||:|||||:|||||:|||||
g678      PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          70      80      90     100     110     120

      130     140     150     160
m678.pep  VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          :|||||:|||||:|||||:|||||:|||||:|||||
g678      IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGCG ACACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACTCTT TGCCGACCC
151 TTCGCCGACA TCGCCTTTCG ATCGTCCAA CCGCGCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51 FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILIIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||
a678      MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ
          10      20      30      40      50      60

      70      80      90     100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||:|||||:|||||:|||||:|||||:|||||:|||||
a678      PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIIITLL
          70      80      90     100     110     120

      130     140     150     160
m678.pep  VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          |||:|||||:|||||:|||||:|||||:|||||
a678      VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA
101 GCCTGCTTGT TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGTTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACT ATTTTCGCAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGCA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTC AATGCAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGAGTTG
301 GCGTTGGTGG TGTTCGCGC GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAACGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACG ATTTTCGCAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPKN TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRF*MXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680       TLCLVLQKTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAELVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

```
g680      |||||::|||||:|||||:|||||:  
          ASLRIGAEKVAEKSRVWRGRSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW  
           130       140       150       160       170       180  
  
          190       200       210       220  
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPNKTVWRSGRFLMX  
          ::|||:||  
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVC RSGRFLMX  
           190       200       210       220
```

a680.seq

1	ATGACGAAGG	GCAGTTCGGC	AATATCCAGC	CCCCGCGCGG	CGATATCGGT
51	GGCGACGAGG	ACGCGCAGGT	TGCCGTCTTT	GAAGGCGTTG	AGTGTTCGA
101	GCCGGCTTTG	TTGGGAACGG	TCGCCGTGTA	TCGCCTGTGC	GGACAGGTTG
151	CGGCGCACCA	GTTGCGCGGT	TACGCGGTGC	ACGCTTTGTT	TGGTTTTGCA
201	GAACACGATG	ACCTGGTTCA	TATGCAAAATC	GACAATCAGC	CGTTCGAGCA
251	GGTTGCGCTT	CTGAATGGTA	TCGACGGCGA	TGATGTGCTG	CTCGACGTTG
301	GCGTTGGTGG	TGTTTGGCG	GGCGACTTCG	ACGGTTTCGG	GCGCGTTTCAT
351	GAAGTCTTGC	GCCAGTTTGC	GTATCGGGGG	GGAGAAGGTG	GCGGAAAAGA
401	GCGAGGTTTG	GCGTTGGCGG	GGCAGCATCT	GCATGATTTT	GCGGATGTCTG
451	TCGATAAAAC	CCATATCCAG	CATACGGTGC	GCTTCGTCCA	AAACGACGAT
501	FTCGACTTTG	TTCAAATGGA	TGTTTTTCTG	TTTCACGTGG	TCGAGCAGCC
551	GTCCGACGGT	GCCGACGACG	ATTTCGCAGC	CGGCACGCAG	GTCGGCGGTC
601	TGTTTGCTCA	TATTCATACC	GCCGAACAAG	ACGGTGTGGC	GCAGCGGCAG
651	GTTTTTGATG	TAG			

a680.pep

1	MTKGSSA	ISS	PRAAISV	TRRLPSL	KAL	SVSSRLC	WER	SPCIACAD	RRL
51	RRTSSRV	TRS	TLCLVLQ	NTM	TWFICKS	TIS	RSSRLRF	*MV	STAMMCC
101	ALVVSCA	ATS	TVSGAFM	KSK	ASLRIGA	EKV	AEKSRV	VWRWR	GSICMIL
151	SIKPISS	IRS	ASSKTTI	STL	FKWMFFC	FTW	SSSRPT	VATT	ISQPARR
201	CLSFIPP	NK	TVWRSG	REFLM	*				

		10	20	30	40	50	60
m680.pep		MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
		: :					
a680		MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
		10	20	30	40	50	60
		70	80	90	100	110	120
m680.pep		TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC					
a680		TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVSCAATSTVSGAFMKSC					
		70	80	90	100	110	120
		130	140	150	160	170	180
m680.pep		ASLRIGA EKVAE KSRVVRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
a680		ASLRIGA EKVAE KSRVVRWRG SICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
		130	140	150	160	170	180
		190	200	210	220		
m680.pep		SSSRPTVATTISQPARSAVCLSFIFPPNKTVWRSGRFLMX					
a680		SSSRPTVATTISQPARSAVCLSFIFPPNKTVWRSGRFLMX					
		190	200	210	220		

g681.seq
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCCAA
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacga

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTGCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCT AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTTCCGCGT TGTGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCCCC GTTTCGAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

g681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGLEEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VFVGVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADEFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

m681.seq

```

1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCT AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

m681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||
g681       MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

1092

```

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDGLECAVFGKLPCAA
          |||||
g681      KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGNGLCAVFGKLPRAA
          |||||

      130      140      150      160      170      180
m681.pep  FGLGEQCGGFRVGFVDGVEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP
          |||||
g681      FGLGKQCGGFRVGFVDGVEADDAEVVGVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP
          |||||

      190      200      210      220      230      239
m681.pep  VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA
          |||||
g681      VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA
          |||||

      190      200      210      220      230      240
m681.pep  LRCFCIFGVWKRIRAVFCGRRX
          |||||
g681      LRCFCIFGVWKRIRAVFCGRRX
          |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTGGG GCGCATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATCCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAATGCGT TTCATTGCGG GAATACGTT. GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1   IITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQOT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFGVLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

```

      10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQOTLSISLPISLV
          |||||
a681      IITPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQOTLSISLPISLV
          |||||

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDGLECAVFGKLPCAA
          |||||
a681      KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA
          |||||

```


	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNNGGFA	VEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVRV	VGVFVGLVAAEET	PAAVVFKNNGGFA	VEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	GNLTGXKLTDFTT	IRALSADGGGLVV	QCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHC	GNLTGXGKLADFT	TILALSADGGGLV	QCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTGACGAT  GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAT  GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT  GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGTTTCC AACTGACCGA
301 CCCATTCCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g682      MRDFAVWVVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY----EMAMPSEPDWIoTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g682      PILILIDYICVNDEIKMPSEPDWIoTAFCMAYGFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||
g682      YPTRSLPKSKKAYGX
          120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
 51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101  TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151  ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201  ATAT.....
251  .....TATA TTCGTTTCC AACTGACCGA
301  CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351  TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
  1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
 51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101  PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

m682/a682  80.6% identity in 129 aa overlap

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWIoTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
          70      80      90      100

      130
m682.pep  LPKSKKAYGX
          |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||
a682      LPKSKKAYGX
          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
  1  ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
 51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101  AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151  GACAGTGTGA GAAAAACGGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201  TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251  CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301  AGTTTCGCTAC AGTTATTGTA TACAAAAAAC ACGGAAATT CCACACAAA
351  CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTACCAAT CTAAAACAAG AACGTTTTGC CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	SSLRPMISLSGLTEKQYETVCGKKLX					
g683	SSLRPMISLSGLTEKQYETVCGKKLX					
	130	140				
m683.pep	SSLRPMISLSGLTEKQYETVCGKKLX					
g683	SSLRPMISLSGLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTACCAAT CTAAAACAAG AACGTTTTGC CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a683      MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
          10      20      30      40      50      60

      70      80      90      100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
          |||||||||||||||||||||||||||||||||||||||||||||||||
a683      IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
          70      80      90      100     110     120

      130     140
m683.pep  SSLRPMISLSGLTEKQYETVCGKKLX
          |||||||||||||||||||||||
a683      SSLRPMISLSGLTEKQYETVCGKKLX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

```

g684.seq
1  ATGCGCCTTT TCCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCAGGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

```

g684.pep
1  MRLFPIAAL TLAACGTVQS TOYFVLPDSR YIRPATQGGE TAVEVRLAEP
51  LKRGGGLVYQT DPYRINTAQN HVWADTLDDM LEAALSNAFN RLDSTRTFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTALE QGLKQAAQOM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

```

m684.seq
1  ATGCGCCTTT TCCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

```

m684.pep
1  MRLFPIAAL SLAACGTVQS TOYFVLPDSR YIRPATQGGE TAVEVRLAEP
51  LKRGGGLVYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTKEW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

```

      10      20      30      40      50      60
m684.pep  MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT
g684      MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT
      10      20      30      40      50      60

      70      80      90     100     110     120
m684.pep  DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS
g684      DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS
      70      80      90     100     110     120

      130     140     150     160     170
m684.pep  YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
g684      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
      130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

```

a684.seq
1  ATGCGCCTCT TCCCGATTGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTGTCG CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGC CGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTGTTCCT
301 GCCTCACGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGTAC GCGGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

```

a684.pep
1  MRLFPAAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGE TAVEVRLAEP
51 LKRGGGLVYQT DPYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTKWT TVYIDAFQGS YTGKTLISGY AVLPDGTNRP FHIETEQQGD
151 GYAAMTAALE QGLKQAAQOM VE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

```

      10      20      30      40      50      60
m684.pep  MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT
a684      MRLFPAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGGLVYQT
      10      20      30      40      50      60

      70      80      90     100     110     120
m684.pep  DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS
a684      DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS
      70      80      90     100     110     120

      130     140     150     160     170

```

```
m684.pép      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
|||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
                130      140      150      160      170
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```
g685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCCT GCCGGCCGCC
151 TGTTGCCCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgtcg ccgtgtAcga CtgggCGGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTGC AGCCTGCATT TGACAAGCGG GCAACCGTGG
401 GGACGCTGTT TGAGCCCGAT TCGGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCTATTA CCGGCGGGCC GGGTGC GGAA GCGTATGAAC AGTTGGCGAA
501 AAACCGGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTTCG CCCAAAAGCG
651 CGAAGCGGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCTG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGCGCAAG TTGGATACAC
751 GGCGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CGGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG
```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

```
g685.pép
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAAST PVATLTVPTA RGDVVVPKNP ERVAVYDWAA
101 LDLTLEPGVN VGATTAPVRV DYLPAPFDKA ATVGTLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNGN IRTSGEKOME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIGQEGPAA
301 VEVLDNAIVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```
m685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTGCCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCCGGCCGG TGCCTGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCTATTAC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCAGAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCGGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGGAAGCGCA AGCAAATCAT
951 CGTCATGCTT GCGCGGAAC ACATTGTCTG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAAGAAAGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pép

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSFAFGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
              |||||
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              |||||
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep      DYLPAPFDKAATVGTLFEPDYEALHRYNPQLVITGGPGEAEYEQ LAKNATTIDLTVDNGN
              |||||
g685           DYLPAPFDKAATVGTLFEPDCESLHRHNPQFVITGGPGEAEYEQ LAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARI FGKEARAAELKAQIDALFAOTREAAKGGKRGVLVSVTGNKVSFAFG
              |||||
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGGKRGVLVSVTGNKVSFAFG
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF EYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||||
g685           TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF EYIKEKNPDWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
              |||||
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGCGCGTGG TTTCTGCAGG
51 TTGTTTGCCT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCGTCCT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGTGGA
351 TTATTTCAGC CTTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCCCG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCAGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAAGCGA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKOMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSFAFGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

m685.pep	10	20	30	40	50	60
a685	10	20	30	40	50	60
m685.pep	70	80	90	100	110	120
a685	70	80	90	100	110	120
m685.pep	130	140	150	160	170	180
a685	130	140	150	160	170	180
m685.pep	190	200	210	220	230	240
a685	190	200	210	220	230	240
m685.pep	250	260	270	280	290	300
a685	250	260	270	280	290	300
m685.pep	310	320	330	340	350	
a685	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTGCGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```


This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS  GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWFPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..

```

1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTGCCTT ACTCCTGCG TCAGCATACT ACCGGCATTG
251 TGGAACGGT CCGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTTTCATCAGA ATCGGAATGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep

```

1  MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	10	20	30	40	50
				40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		70	80	90	100	110
		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
g686.pep		100	110	120	130	
		GIAAALWFPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
m686		130	140	150	160	
		GIAAALWFPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)

```

1  ..AATTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GGCAGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGTCAGCA TACTACCGGT
151 ATTGTGGAAG CCGTCGACAA GCCGTGTGCC GGTGCTGCGG TTGTGCGTCA
201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51 IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAALWFPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDDICSAVEGFGGIARSVQLG
a686                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
                NFSCRADDVFNDDICSAVESFGGIARSVQLG
                      10      20      30

              70      80      90      100     110     120
m686.pep    AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
                AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                      40      50      60      70      80      90

              130     140     150     160
m686.pep    GIAALWFPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
                GIAALWFPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
                      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCCG CCCTGTTCCG
51  CCTTGCCGCG TCGGACAGCA AAGTCCAAAC CAGCGTCCCC GCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCGCCCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTTCG GCTATTTTTC TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
351 cGCGCCGCGC GTCGATATGG CTGCCGCGCA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAA ACcgccctTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGCGGCGA AATATAAAGT CGAATTGCGC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGO
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWVQKE MLPLARLAAA VDMAAESKD VANSHIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGGCGCTG
101 CCGCTTCGGC AGCCGCGGCC CCGGCAGGGC TGGTCGAAGG GCAAAACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

1103

```

501 TGCCGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
  1 MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

m687/g687 97.0% identity in 234 aa overlap

```

          10      20      30      40      50
m687.pep  MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||
g687       MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

          60      70      80      90      100     110
m687.pep  QQQAGKVEVLEFFGYFCPHCAHLEPVL SKHAKSFKDDMYL RTEHVWVQKEMLTLARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||
g687       QQQAGKVEVLEFFGYFCPHCARLEPVL SKHAKSFKDDMYL RTEHVWVQKEMLPLARLAAA
          70      80      90      100     110     120

          120     130     140     150     160     170
m687.pep  VDMAAADSKDVANSHIFDAMVNQKIKLQNPV LKKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||
g687       VDMAAASKDVANSHIFDAMVNQKIKLQEPV LKKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

          180     190     200     210     220     230
m687.pep  ADKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |  |||||  |||||  |||||  |||||  |||||
g687       AGKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
  1 ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
 51 CGCGTGCGAC AGCAAAGTCC AAACAGCGT CCGCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
  1 MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N. meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIPQQ					
a687	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIPQQ					
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
a687	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLKWLGEQTAFDGKKVLAAYESPESQARAD					
m687.pep	190	200	210	220	230	
	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAOX					
a687	190	200	210	220	230	
	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGTCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAQKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGTCACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCCTGTTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPYRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

	10	20	30	40	50	60
m688.pep	VLHYP	SRFAQ	KGISV	NKTLI	LALSALL	GLAACSA
g688	VLHXT	SRFAQ	KGSPV	NKTLI	LALSALL	GSLTACSV
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGM	TKDQV	LLLLG	SPILR	DAFHT	DRWDYTF
g688	LRPGM	TKDQV	LLLLG	SPILR	DAFHT	DRWDYTF
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQN	AEEAL	KDRQNT	DKPX		
g688	DALQN	AEEAL	RAKQNA	DKQX		
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

a688.seq

1	GTGTT	ACTACT	ACCCAT	CCCCG	ATTGCA	CACAG	AAAGGC	ATTTC	CCGTGA	AACAA
51	AACCTC	ATCCT	CGCCCT	CTTCC	CGGCCT	TGCG	GCGTGC	AGCG		
101	TCGAAC	GCGGT	TTCAC	TGTTT	CCCTCG	TACA	AACTCA	AAATC	CATAC	AGGGC
151	AACGA	ACTCG	AACCT	CGCGC	CGTCGC	CCTCC	CGCCCG	GTATG	ACCAA	
201	AGACCA	AAGTC	CTGCT	CCTGC	TCGGCA	GCCCC	CATACT	GCGC	GACGC	ATTCC
251	ATACCG	ACCG	CTGGG	ACTAT	ACCTTC	AACA	CCTCCG	CAAC	CGGC	ATCATC
301	AAAGAC	CGGAA	GCAAT	CTGAC	CGTCT	ATTTT	GAAAAC	GGCG	TGCTC	GTCGG
351	CACCGA	AGGC	AACGC	CTGC	AAAAT	GCCGC	CGAAGC	CCCTC	CGCGT	AAAAC
401	AAAACG	CAGA	CAACA	ATAA						

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

a688.pep

1	VLHYP	SRFAQ	KGISV	NKTLI	LALSALL	GLAACS	VERVSLF	PSYKL	KIIQG
51	NELEP	RAVAS	LRPGM	TKDQV	LLLLG	SPILR	DAFHT	DRWDY	TFNTSR
101	KDRSN	LTVEF	ENGVL	VRTEG	NALQN	AEEAL	RVKQN	ADKQ*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

	10	20	30	40	50	60
m688.pep	VLHYP	SRFAQ	KGISV	NKTLI	LALSALL	GLAACSA
a688	VLHYP	SRFAQ	KGISV	NKTLI	LALSALL	GLAACSV
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGM	TKDQV	LLLLG	SPILR	DAFHT	DRWDYTF
a688	LRPGM	TKDQV	LLLLG	SPILR	DAFHT	DRWDYTF
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQN	AEEAL	KDRQNT	DKPX		
a688	NALQN	AEEAL	RVKQNA	DKQX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```
1 ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51 GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
101 TTCCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCGAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGGCGAG GCATGGCTGT
351 AGTCATCGTc ggtgcatgg tgcgcatTA TTATTCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GGCGGGCGAT
501 TTTTCGTTTTT ttggcGgcat ATTGCGCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTGCCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601 GGGCTGCTGG CGGGGCGGTT CAAGCGCGTA TGTAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTGAGCTT CGGTTTCGATG TTCGCCCTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCAGT TACGCCGCAC
751 CGGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAAGACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCTGCGT
951 GATGTTTTCC GTCGCTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCGGTGTCG
1051 GGTGTTATCC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CCGCAACCGT
1101 GATGCGGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAAA GCGAATACTT
```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```
1 ..SPPLPPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51 SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLNLRVAVQA FGAGMAVIV GAMVRDYYSG RKAQMFLALI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPV LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFOAFSFGSM FAFLETSSFV YRQLYHVTPH
251 RYAVVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFANPSOLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```
1 TTGTAAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51 GTTGCCGCCT GTTGTGCGG GTGTGTTAAA ATTTCCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTTATG
151 CTTCTGCCC ATTATCCTGA AATGAGCGAA AACTGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTGTGTTAT GTTCGGCAGC GCCTTCGGAC AGGTGGTCGG
351 CGGTTTCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CGGGCATGAC
501 TGTGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGCACGAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGTTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCGTGCTGCT
801 GATGGGTTAT CTGTTTTTTC AGGCATTCAG CTTGCGTTCT ATGTTTCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTACGCTT
901 CATCAATACG CTTGGGCGGT TGCACCTAAC ATCATCACA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCGT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTT GTCCCAACTC
1051 GCCGCGGTGC TGTTTTTGCG GTTGCCCGCG TTTGGCTGCT TGGTCGCTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGACAG
1151 CGTGTGTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGCAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGGC TCTGCTCGCA TCGTGGCTGG
```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep

```

1  LLIHVIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH POSILLWGIV VOFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSSIDA					
g689						
				SPPLPPMSGKLMMAVLMVALMPFSIDAY		
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLNLRAVQAFGAGMAVVIVGAMVRDYYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFRKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFVSVGTQGLVGAD					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFVSVGTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360		370	380
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

a689.seq

```

1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTGTGCGCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCCA AATGGCGCAG TCGTGAACG CCGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCCG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGTCTA CTGCCCTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCCGCGCAA TGGTGCGCGA TTATTATTC GGACGCAAAG
551 CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAA CCCGTGCCGC
801 GATGGGTAT CTGTTTTTTC AGGCATTAG CTTCGGTTCG ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAG AGCTCTACCA CGTTACGCCG
901 CACCACTAGC CTTGGGCGTT TGCACCTAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAC CCGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTT CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGGTGC AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGACAC GACGGTTCGG CAACCGTGAT GCGCGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

a689.pep

```

1   LLIHIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESS VYQQLYHVTP
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FV FLAAYSLVLLGLVQYFLPKP					


```

a689      |||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSILVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVTP
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVFFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLG VFSQLIGAGVGM AATFLH
          |||||
a689      FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLG VFSQLIGAGVGM AATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
          |||||
a689      DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAAC CGATTTGCAA
151 CCGGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCCGCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAA CCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGC GgCaAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTGAAAG TTTCGGCAAC ATCtgCctat
601 TTgaaccggc ACAaCaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCCGG TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1  MKNKTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHOKIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEFPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPKPFPLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTG CAT
101 CCGCTGCTTC GTCTCCGCG TCATCAGCTC CTTCCCAAAC CGATTTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCACGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACC CGC GgCaAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQOIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHEMLE NQSLFRLSNR ERNPKPFELD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

m690.pep      10      20      30      40      50      60
MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
g690           10      20      30      40      50      60
MKNKTSSLLPLWLAAILAARSPSKEDKTKENGASAASSSASSQTDLQPAASAPDNVK

m690.pep      70      80      90      100     110     120
QAESAPPSNCTSLHPATGIDDLMQOIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
g690           70      80      90      100     110     120
QAESAPLXNCTGLHPAAGIGDLIQOIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL

m690.pep      130     140     150     160     170     180
LFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690           130     140     150     160     170     180
LFPDIRPEDPDYHQKIMLAIEDLRYGRTISRQAQDAIMEQERRLREATLMLTQGSQKTR

m690.pep      190     200     210     220     230     240
GQGEPEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHEMLENQSLFRLSNR
g690           190     200     210     220     230     240
GQGEPEPKRTRYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMHGEMLNQSLFRLSNR

m690.pep      250     260     270     279
ERNPKPFELDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690           250     260     270
ERNPKPFELDIHFDENGKITRIVVYEKNIY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCCTC GTCCACGGCA TCCGCCGCTT CGTCTTCCGC GCCCAAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT  AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC  GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCCG CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCAGCGGTT ATTTTGAAAT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT  ACACGGAGAA ATGCTTGAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPKDP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
a690	10	20	30	40	50
m690.pep	60	70	80	90	100
a690	60	70	80	90	100
m690.pep	110	120	130	140	150
a690	110	120	130	140	150
m690.pep	160	170	180	190	200
a690	160	170	180	190	200
m690.pep	210	220	230	240	250
a690	210	220	230	240	250
m690.pep	260	270	280	290	300
a690	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCGCTGCT CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAA ATCCGCGCCG CCTTCAAAAT
 201 GCGGGCGGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAATG GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGOHNELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GCGGCTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGGCGGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
      |||
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
      |||

      10      20      30      40      50      60
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||

      70      80      90     100     110     120
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||

      70      80      90     100     110     120
m691.pep IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
      |||

      130     140
m691.pep EIQRFFHILTPQQQMWLS SCLKX
      |||
g691      EIQRFFHILTPQQQMWLS SCLKX
      |||
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GTCGCTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGGCGGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDPQPCNDIRRLGLTQSOHNELRK					
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDFQPCNDIRRLGLTQGOHNELRK					
	10	20	30	40	50	60
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
a691	IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
m691.pep	EIQHRFFHILTPQQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

1	GTATCGCACA	CACGCTGTCG	CTGTTCCGAA	TCGAtacGCC	GGATTGCGC
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATGCGGTTCA	GACGGCATCA	TTTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGT	ATTTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTgacGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGCTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTGCGCGGC
401	AGTTGTGCGG	CTTCAAGCTC	GACGATTTTG	ATGTTTTTCA	GGTTTTCCGC
451	GATGTGCGCT	TTGGATGCGG	TCAGCGGATT	GATGCCGTCT	TTGAGTTTGA
501	TCCAACCCAG	TTCGTTTCAGC	ATCACCAAGG	CGCGTCCGAA	GTTGGAcggG
551	TcgtTGGGCG	CGGATACGGT	GCTGCCGTCT	TTGACTTCTT	CCAGCGATTT
601	CAGTTTCCCC	GGATACAGTC	CCAAAGGCGC	GGTCGGCACT	TGGAAGGCTT
651	CGGTGATGTC	CAGGTTGTGT	TCTTTTTTGA	AATCGTCAAG	ATAGGGTTTG
701	TGTTGGGAAGA	CGTTGATGTC	CAACTCGCCC	TCCGCCAATG	CCAGATTCGG
751	GCGCACATAG	TCggTAAATT	cgaccaatTT	gacgGTGTag	cCTTTTTTCT
801	CCAGCTCGgc	tTGGATTTGT	TCTTTGACCA	TATcgccgaa	gtcgccacg
851	gTCGTGCCGA	agacgaTTTC	TTTTTTCGc	GgcCGTTAT	CGGCAGAAGG
901	GGCGGCGgca	gaggctgcGG	GCGCGCTGTC	TTTTtgaccG	ccgCAGGCTG
951	CGAGGATGAG	CGCGAGtgcg	gcggcgga	ggGTTTTGAA	GAAGGTTTTc
1001	atATTTTCTc	ctga			

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g692.pep

1	VSHTRCRCSE	SIRRIWRNGR	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA
51	FIPCGRVFVA	LEAFVRVGF	RVGVIGLV	FKPLAVFVGG	FDGRPVDIGK
101	ARLLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	AARQLCGFKL	DDFDVFQVFR
151	DVGFGCGQRI	DAVFEDPTQ	FVQHHQGACE	VGRVVGGRYG	AAVFDFQRF
201	QFARIQSQR	GRHLEGFQDV	QVVFVEIVK	IGFVLEDVDV	QLALRQCQIR
251	AHIVGKFDQF	DGVAFFLQLG	LDLFFDHIAE	VAHGAEEDDF	FFRAVIGRR
301	GGRGCGRAV	FLTAAGCEDE	RECCKGKGF	EGFHIFS*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

1	GTGTTGCACA	CGCTTTGTCG	CTGTTCCGAA	TCGATACGCC	GGATTGCGCG
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATACAGTTCA	GACGGCATCA	TTTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGG	ATTTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTGACGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGTTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTACGCGGC

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGCGAGC ATCACCAAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGTTTGA
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVRFCCGQRI DAVFEFDEPTO FVEHHQDAGE VGRVVRGYYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAV LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
g692	VSHTRCRCSE	SIRRIWRNGR	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA	FIPCGRVFVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVIGLGYV	FKPLAVFVGG	FDGRPVDIGK	ARFLEQGFQ	LHAAYGVVA
g692	LEAFVRVGF	ERVGVIGLGYV	FKPLAVFVGG	FDGRPVDIGK	ARFLEQGFQ	LHAAYGVVA
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	AATRLRGFKL	DDFVQVLG	DVRFCCGQRI	DAVFEFDEPTO	FVEHHQDAGE
g692	VDDGKIHVGA	AARQLCGFKL	DDFVQVFR	DVGFCCGQRI	DAVFEFDEPTO	FVQHHQGACE
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVRGYYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
g692	VGRVVRGYYG	AAVDFDFQRF	QFARIQSQR	GRHLEGFQDV	QVFFFEIVK	IGFVLEDVDV
	190	200	210	220	230	240
	250	260	270	280	290	
m692.pep	QLALSQCQIR	AYIVGKLDQF	DGAFFLQLGL	DLFFDHIAE	VADGRAEDDF	FFRAVVG--
g692	QLALRQCQIR	AHIVGKFDQF	DGAFFLQLGL	DLFFDHIAE	VAHGRAEDDF	FFRAVIGRR
	250	260	270	280	290	300
	300	310	320	330		
m692.pep	GGRSGCGGRA	VFLTAAGGEDER	ECGGGKGFE	EGFHIFSX		
g692	GGRSGCG-RA	VFLTAAGCEDER	ECGGGKGFE	EGFHIFSX		
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGCACT TGAAGACTT
651 CCGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTTGT TCTTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGCAGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1  VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGFV RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVQVG
151 NVRFGCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVRGGRY AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFFEE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

```

              10      20      30      40      50      60
m692.pep     VLHTLCRCSESIRRIIRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFIPCGRGFVA
              |||||
a692          VLHTLCRCSESIRRIIRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFIPCGRGFVA
              10      20      30      40      50      60

              70      80      90     100     110     120
m692.pep     LEAFVRVGFERVGVIGLVFKPLAVFVGGFDFGRPVDIGKARFLEQGFQQLHAAAYGVVA
              |||||
a692          LEAFVRVGFERVGVIGLVFKPLAVFVGGFDFGRPVDIGKARFLEQGFQQLHAAAYGVVA
              70      80      90     100     110     120

              130     140     150     160     170     180
m692.pep     VDDGKIHVGAATRQLRGFKLDDFDVQVLGDFVFGCGQRIDAVFEFDPTQFVEHHQDAGE
              |||||
a692          VDDGKIHVGAATRQLRGFKLDDFDVQVFGNVRFGCGQRIDAVFEFDPTQFVEHHQDAGE
              130     140     150     160     170     180

              190     200     210     220     230     240
m692.pep     VGRVVRGRYGA AVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
              |||||
a692          VGRVVRGRYGA AVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
              190     200     210     220     230     240

              250     260     270     280     290     300
m692.pep     QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFFRRAVVGGG
              |||||
a692          QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFFRRAVVGGG
              250     260     270     280     290     300

              310     320     330
m692.pep     RSGCGGRAVFLTAAGGEDERECEGGGKGFEFGFHIFSX
              |||||
a692          RSGCGGRAIFLTAAGGEDERECEGGGKGFEFGFHIFSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

g694.seq

```

1 TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51 AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCTATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GcaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGACTGTT CGGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTTCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCATTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCGCGT TCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGCGCGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 CGGCACATAA ACCGGCGCGC CGAATTCCTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTC CGTTCATAAG TTTTGCATTG CGTGTTCAGA CGGCATTCAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

g694.pep (partial)

```

1 SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPFAHG
51 FMPPSAYGCG YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHOR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDDEV
301 AHINRRAEFF QSTFDNTDCP IHTGAEEAARI GKDDGFSVHK FCIPCSGDIH
351 VFLLXCDGR YCQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

m694.seq

```

1 TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51 GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTGCTCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAATCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCAGC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

m694.pep

```

1 LVASASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGODE
51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV

```



```

151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

m694.pep      10      20      30      40      50
LVSASGTRQKCR LKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694          10      20      30      40
SAFVLPKHPMPAL TPASTFAQIGFGFALAAQLLGQDEHDAFFR

m694.pep      60      70      80      90     100     110
TLAFAYGEVPPS AYGCQYFPHQHFGGRGRACRYADVFV FALKPCALQVACIIHHRIDSARC
g694          50      60      70      80      90     100
APPFAGHGFMPPS AYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHRIDSARC

m694.pep     120     130     140     150     160     170
RHFAQAVAVGRIG RTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694         110     120     130     140     150     160
RHFAQAVAVGRIG RTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV

m694.pep     180     190     200     210     220     230
FGFIDRERGLADIG EFVGVSDFEFCHISDRFDQKH FARRKLPHRSFDLDVPLMPDHDDFT
g694         170     180     190     200     210     220
FGFIDRERGLADIG EFVGVSDFEFCHISDRFDQKH FARCKLPHRAFDLGVLMPDHDDFT

m694.pep     240     250     260     270     280     290
VLGIQSGDFLMHFR HQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694         230     240     250     260     270     280
VLGIQSGDFLMHFR HQRASRIKYPETALRRFLHLRLRYAVCRINQCRARRHFRQVFDKHR

m694.pep     300     310     320     330     340     350
TFFTQVVHDEFVFN DVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694         290     300     310     320     330     340
AFFAQVVHDEFVVD DVAHINRRAEFFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI

m694.pep     360     370     380
SFSDGINIFLLGFY GGRCCPTPPTPHRRRX
g694         350     360     370
PCSDGIHVFLXXLCD GRYCQAPPTPHRRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1  TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGCAATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG

```

```
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGTTGTGTC ACACGAAT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCTC
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```
a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRIADI FLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

```
m694/a694 100.0% identity in 385 aa overlap

      10      20      30      40      50      60
m694.pep LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
a694      LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
      10      20      30      40      50      60

      70      80      90     100     110     120
m694.pep AYGFVPPSAYGCQYFPHQHFRGRACRYADVFVALKPCALQVACIIHHIRIDSARCRHFA
a694      AYGFVPPSAYGCQYFPHQHFRGRACRYADVFVALKPCALQVACIIHHIRIDSARCRHFA
      70      80      90     100     110     120

      130     140     150     160     170     180
m694.pep QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRADI FLVRIADIGETRVQRGDDVFGFI
a694      QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRADI FLVRIADIGETRVQRGDDVFGFI
      130     140     150     160     170     180

      190     200     210     220     230     240
m694.pep DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
a694      DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
      190     200     210     220     230     240

      250     260     270     280     290     300
m694.pep QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
a694      QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
      250     260     270     280     290     300

      310     320     330     340     350     360
m694.pep QVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
a694      QVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
      310     320     330     340     350     360

      370     380
m694.pep GINIFLLGFYGGRCCTPPTPHRRRX
a694      GINIFLLGFYGGRCCTPPTPHRRRX
      370     380
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCACAT ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCGG AGGGCAGCCG AACCAGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACCGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1   LPQTRPARRH HRHROYFVER KGDARSGF*C AAQCONSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCACAT ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCGG CAGGCAGCCA AACCAGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1   LPQTRPSRRH HRHROYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHRRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR					
g695	10	20	30	40	50	60
	LPQTRPARRHRRHRRQYFVERKGDARSGFXCAAQCONSQRQFQSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIIWLSVSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	70	80	90	100	110	120
	FDPASEKIMKTKLPLFIIWLSVSVSASCASVLPVPEGSRTMPTQENASDGIPYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRLKKEHYLNTTEGGSASA					
g695	130	140	150	160	170	180
	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDDRLKKEHYLNTTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSIQRSMYLLQLSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKAAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKAAA					
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTTGTCCGGC	AAGGCGGCAT	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCCAGC
101	GTCGGCATCC	TCAAAGATTT	TAATCAAAAC	CTGCCGAACG	ATACGCCGAT
151	TGTCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCCTG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTTGGCTG	TCCGTATCCG
251	CCGCCTGTT	TTCCTGTT	TCCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTGCA
401	ACGAAGTGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCAATGCGAAA
451	ACACACCCTT	CCAGCAGGGC	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAAGC
601	GGCAGTTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGGCGGCAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHFPARRR	FDPASEKIMK	TKLPLFIIWL	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRLKKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQOKDIAR	ATWRSLIQTY	PGSPAARKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPORFQSKPAERPAHRPHHPARRRR					
a695	LPQACPARRHCHROQYFVERKGDARSGFRCAAQRRHPORFXSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	
m695.pep	LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQT---EMSTRENASDGIYPVPVPTL					
a695	FDPASEKIMKTKLPLFIWLSVSAACSS--PVS RN IQDMRLEPQAEAGSSDAIYPVPVPTL					
	70	80	90	100	110	
	120	130	140	150	160	170
m695.pep	QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYL NTEGGS					
a695	QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYL NTEGGS					
	120	130	140	150	160	170
	180	190	200	210	220	230
m695.pep	ASAHTVETAQONLYNQALKHYKSGKFSAAASLLKGADGGDGGSIQRSMYLLQLSRARMGN					
a695	ASAHTVETAQONLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQLSRARMGN					
	180	190	200	210	220	230
	240	250	260	270	280	290
m695.pep	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRS LIQTYPGSPA AKR					
a695	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRS LIQTYPGSPA AKR					
	240	250	260	270	280	290
	300					
m695.pep	AAAAVRKRKX					
a695	AAAAVRKRKX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence <ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

1	TTGGGTTGCC	GGCAGGCGGC	ATCCCATCAT	TTTGGCCAAG	GCAACAAATT
51	ATTTGGCGGC	ATCTTTCATT	TTGTCTGCCG	CTTCCTGAGT	CGCGTCGGCA
101	GCTTTGTTCA	AAGTATCTTT	AGCTGCTTCA	GTTACAGCTT	CTTTGGCTTC
151	AGTTACAGCT	TCCTCGGCAC	TTGCCTTTGC	ATCAGCCGCA	GCATCTTTGA
201	CTTGGTCTTT	CGCTTCTTCG	ACGGCAGAAG	CGGCAGACTC	GGCGGCAGAA
251	GCCGCACTGT	CTTTAACATC	GGACTCAACG	GCTTGAACCG	CTTCCTTAAC
301	CTCCTGTTTG	GCTTCTTGCG	AACAAGCTGC	CAAGGCAGCC	GCCATCATTG
351	CGGCAATCAA	TAA			

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

1	LGCRAASHH	FCQGNKLF	GGIFHFVCRFLS	RVGSFVQSIF	SCFSYSFFGF
51	SYSFLGTCLC	ISRSIFDLVF	RFFDGRSGRL	GGRSRSVFNI	GLNGLNRFLN
101	LLFGFLRTSC	QGSRRHCGNQ	*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFNL
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

m696.pep      10      20      30      40      50      60
               LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
               |||||
a696           10      20      30      40      50      60
               LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
               |||||

m696.pep      70      80      90      100     110     120
               ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFNL
               |||||
a696           70      80      90      100     110     120
               ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFNL
               |||||

m696.pep      X
               |
a696           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTTCG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGGC GATATGGCGT TGACGGTTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTAATGACCG AGGCTTACCG
651 GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC GGATGCGGCG
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTCCGGGC GGTTTGGAAG TCGTGCCGCT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCCG TTTCTGATGG TGGTGTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSM DFTLPVIQAG GLEVPVAVS FGVVNVIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

```

1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCGGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCT
151 CCGGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATTCGGC AAACGTATGC GCGATATTG GATGCCGCT GAAAGCGCGG
401 GCATGTATTG TCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
501 GTTGTCCGTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTGTTTG
551 CCGCATCGAC AGACGGTGTG TCGTGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTCATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTCC AGATGCGGCG
751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATGCG CCGTGATTCA
801 GGGTGCGGGC GGTGTTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CGCTTTGGGT
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

```

1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLF PWRIKKGKGV
101 VGVSGSVGQL GCVLLGFAGF KLMRDIWMP ESAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS
201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSM DFTLPVIQAG GLEVPVAVS FGVVNVIAAP FLMVVFSA
301 *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLF PWRIKKGKGVSVGVSGSVGQLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLS PWRIKKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPLVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPLVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGTGTGTG CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCAATCCGG AAACGTATGC GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCG
501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GTATATCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTATTCGG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGGTGCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCTG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGCGGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTT CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPP RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMDIWMPS ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSLGL VMTEAYGAVW GSIALLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPPRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLFPPRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMDIWMPSSEAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMDIWMPSSEAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180
m700.pep	KLMDIWMPSSEAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMDIWMPSSEAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIALLLNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAAACCTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCTGTC GCGGACACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG
51  FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC SGTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPEAGLMVWVAPNSFAS	FKRFSISQT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVWVAPNSFAG	FKRFSISHT			

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```

          10      20      30      40      50      60
          70      80      90     100     110     120
m701.pep  MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG
          :|||||:|||||:|||||:|||||:|||||:|||||
g701      IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC
          70      80      90     100     110     120

          129
m701.pep  SGTRLLSAX
          :|||||
g701      GGTRLLSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```

a701.seq
  1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
 51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101  CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151  TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201  CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251  TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301  TGTGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351  GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```

a701.pep
  1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
 51  FKRFSISQST MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101  CAVGKASLNN RATSSLTLSG SGTRLLSA*

```

m701/a701 92.2% identity in 128 aa overlap

```

          10      20      30      40      50      60
m701.pep  MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQST
          |||||:|||||:|||||:|||||:|||||:|||||
a701      MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSISQST
          10      20      30      40      50      60

          70      80      90     100     110     120
m701.pep  MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG
          |||||:|||||:|||||:|||||:|||||:|||||
a701      MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSC
          70      80      90     100     110     120

          129
m701.pep  SGTRLLSAX
          :|||||
a701      SGTRLLSAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```

g702.seq
  1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
 51  AATCAGGGGA ATGCCGTGT TGCGGCCGCG TCTGGCGAGG GATTCTGTGCA
101  AACC CGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151  TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201  TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251  TTTGAGGGT GGGGATGCCG CTTTCGACAA GGGCGCGGGA CAAATCGACG
301  GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAATG CGCCGGCGGT
351  CAGGATTTTCG cgggggtca gttga

```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCCAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP					
g702	MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCKPGLMAKTAPASSTALSCSGLVTVPPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAITGTTAPAVKIS					
	:					
g702	MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVLRVEWGILLRWDRXL					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCCAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDR LX
          |||||||||||||||||||
a702      RGVSLDISVLRVEWGILLRWDR LX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTGc gctGTTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVND SREV
251 KVPSFDEMKG QIAGNLQAE R IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

```

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGVVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVAAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTGCGGAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCCTCCTT CAAAACCGTT TGGCAGGCGG TAAATATATGG
351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREVS
251 KVPSFDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNDREVSREVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
a703	VYYVNDREVSREVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCGC TGCCGACCTA CCTTTACGGC
601 GGCGACATCG AACCCGATTT CTGCAAAATC CTCCATTGGG GCGGCTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701 CGGTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```
801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCG ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGGCG
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCTCG CCCAAACCAAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAAA CAGAAGGCGG
1851 GCGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CAATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAATGCCG TCCGAACAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```
a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS I IDAGLGSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLLRDGI V RIDLNYSTHR CRVWDDGKI RLS DILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALEPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFYCAVPF YQGAIRD LKN RRVGMDPTIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DQOETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALAEQYAS SFIFGELL LLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEA VRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLG YVQPIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*
```

m704/a704 99.8% identity in 823 aa overlap

```
105 20 30 40 50 60
m704.pep MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
|||||
a704 MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
10 20 30 40 50 60

70 80 90 100 110 120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDGI
|||||
a704 ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDGI
```

1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA				
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVLVPPVFCYCAVPFYQGALRDLKN				
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSLATNAGQGM	YFESIAMLFFLLGGRFMEHIARRKAGD				
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLI	PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV				
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSP	LIIRTDRTGGGTRL	SHIVRL	LDRALAQKPR		
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAEAEQYASSFIFGELL	LAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL				
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTTD	IIFDKTGTLTQGKPAVRRISLLRGTD	EAFLA			
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPD	IAIKQRLNRIGEGVGAQLTVNGETQVWALGR				
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYLSQSGFQ	AVFYLTDP	LKDSAAEAVRQLAGKNLTLHIL			
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGV	AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD				
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRT	VAHLLDQARRTRHII	RQNLWAGAYNII	AVPLA		
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSSLAVLGNALRLH	KRGKMQSEKMPSEQX				
	790	800	810	820		

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

BNSDOCID: <WO 9857280A2 | >

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100     110     120
m705.pep  ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180
g705      ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230     239
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGGC GATTATGCCG GCCGGCGGCA TCGTGCAGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTC
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDFIPAAI IGFSNLVNGAY ASETIRAAIL SVKPGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RAVVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFRDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep  10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||

a705.pep  70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||
m705      70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||

a705.pep  130     140     150     160     170     180
ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||
m705      130     140     150     160     170     180
ASETIRAAILSVKPGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||

a705.pep  190     200     210     220     230     239
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||
m705      190     200     210     220     230
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAatgaCCGT CTTCGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cggtgGAacg taTgctcggg acggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTAttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCCGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCCG
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAAGC TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TCGGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRKRLS GRWLNSYERY RHRLIHAVR LGGTVLFFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLGSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCCGCAAAA ACGGCTACGT CCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAAGC CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TCGGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLGSEIRLL DRHFTLLQTD LQQTVALING

```

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE ROHLRQSLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQKRRLSGRWLSYERYRHRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTSALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTSALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAIEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMAIEISNGRRMTRERLEQNMVKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLOSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTTELLLTAAKLOSPKLNSEIRLLDRHFTLLQTDLQQTAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	ROHLRQSLE TREHGX					
g706	ROHLRQSLE TREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCC CGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCCG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751	CGTAAATTTG	TCAACACCAC	CGAGTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTGCGCCT	TATCAACGGC

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLIFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWFD SG
151 LMRAMNVLIG AAIATAA AKL LPLKSTLMWR FMLADNLDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQH AH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNM RQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

```

a706.pep      10      20      30      40      50      60
MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG
EWIGMTVFVV
|||||
m706          10      20      30      40      50      60
MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG
EWIGMTVFVV
|||||

a706.pep      70      80      90      100     110     120
LGMLQFOGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLT
VGTSALAGWAA
|||||
m706          70      80      90      100     110     120
LGMLQFOGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLT
VGTSALAGWAA
|||||

a706.pep     130     140     150     160     170     180
VGKNGYVPM LAGLTMCMLIGDNGSEWFD SGLMRAMNVLIGAAIAIAA
AKLLPLKSTLMWR
|||||
m706         130     140     150     160     170     180
VGKNGYVPM LAGLTMCMLIGDNGSEWLD SGLMRAMNVLIGAAIAIAA
AKLLPLKSTLMWR
|||||

a706.pep     190     200     210     220     230     240
FMLADNLDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS
HLAATSGESRISP
|||||
m706         190     200     210     220     230     240
FMLADNLDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS
HLAATSGESRISP
|||||

a706.pep     250     260     270     280     290     300
AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQ
TDLQQTVALING
|||||
m706         250     260     270     280     290     300
AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQ
TDLQQTVALING
|||||

a706.pep     310     320     330     340     350     360
RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNM RQE ISALVILLQR
TRRKWLDAHE
|||||
m706         310     320     330     340     350     360
RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNM RQE ISALVILLQR
TRRKWLDAHE
|||||

a706.pep      370
RQHLRQSLLETREHSX
|||||
m706          370
RQHLRQSLLETREHG
X

```

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```
1 ATGGAAATTA TTAACGATGC AGAAGTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAA CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGCG AGCAGAATAA ACCCATACGG TCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTT ATATGGACGC
751 GGTTTGCGCG ACAAACGGA CTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTC TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCGGAG CGCATGCTTT GGCCTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCGC CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGC CATGCCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCGGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAAGAGG GGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTT
1601 CCGCAAGGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```
1 MEIINDAELI RSMQRQOHID AELLTDANVR FEOPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQL
101 IVRGYLTSQA IIQPNMDSG ILKLRVSAGE IGDRIYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUI SEEKGSDLO
201 IKWQONKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQWNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```
1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAAATCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAAACC TGCGTCGTTT GCCGAGTGT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCAAG ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG
```

```
751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```
a707.pep
1   XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNXKPLYRNK ILNLRDVEQG
101 LENLRLRPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYGKQ YQSSLAERM
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHRLAYL
301 RWQLDGKLSY KRGTMGRQSM PAPEENGSGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAOWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

a707/m707 95.3% identity in 486 aa overlap

```
a707.pep
10 20 30
XKETAFTKGMCLGSNNLSRLQKAAQQILIV
|||||
m707
50 60 70 80 90 100
EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIV

a707.pep
40 50 60 70 80 90
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
|||||
m707
110 120 130 140 150 160
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDGKSAEGSISAFNNKFPLYRNKI

a707.pep
100 110 120 130 140 150
LNLRDVEQGLNLRRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||||
m707
170 180 190 200 210 220
LNLRDVEQGLNLRRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT

a707.pep
160 170 180 190 200 210
GKYQGNVALSXDNPLGLSDXFFVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||||
m707
230 240 250 260 270 280
GKYQGNVALSFDNPLGLSDLFVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK

a707.pep
220 230 240 250 260 270
WLFSFNHNGHRYHEATEGYSVNYDYGKQYQSSLAERM LWXXXFXXTSVXMKLWTRQTY
|||||
m707
290 300 310 320 330 340
WLFSFNHNGHRYHEATEGYSVNYDYGKQYQSSLAERM LWRNRLHKT SVGMKLWTRQTY

a707.pep
280 290 300 310 320 330
KYIDDAEIEVQRRRSAGWEAELRHRLAYLXRWQLDGKLSYKRGTMGRQSM PAPEENGSGTI
|||||
m707
350 360 370 380 390 400
KYIDDAEIEVQRRRSAGWEAELRHRLAYLNRWQLDGKLSYKRGTMGRQSM PAPEENGSDIL
```

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQOFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
          | : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      PGTSRMKIITASLDAAAPFILGKQOFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK
          ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTGCGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CTGCGCAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAATTTT CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGO
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLVNDKAO ESFRQALSIE
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPFAFKE LARTKMLAGQ LGDADYYFFK
201 YQSRVEVLQA DDLILGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGAACCC
201 TAAAAACGAG CTGCGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CTGCGCAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTT CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAOESFRQALSIKPDSDAEINNNYGWFLCGRLNR
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAOESFRQALSIKPDSDAEINNNYGWFLCGRLNR
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFPAFKE
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFPAFKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

a708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGCGAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCGAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCCTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

a708.pep

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYXP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPFPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIYQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIIYQYLKVNDKAQESFRQALSIPKPSAEINNXYGWFLCGRNLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFPAFKE					
m708	PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTCGTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGG	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGATA	TGGGCGCGGT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	GCGCGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCGGACT	TATTTTATT	TTTCCGCCTT
351	CGCGCTGTGT	TCCGTATCCG	GCGTGTCCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGGCGTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg	cgcgattgTT	tcgggTGTGT	TTTTCGGCGA
501	TAAAATGTCC	CCGCTTCCG	ACACCACGGG	CATTTCGCG	TCCATCGTCG
551	GTATCGACCT	GTTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	GCGTGCGTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGACGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GACGCGCTAT	TCGCTGATTG	CGTTTGCACT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCCGTAACGT	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTATGGC	GGCTACAAAC	TCGAAGGCGA	AGCGTTTAA
901	GACATTGCCA	AACTGATTTC	GCGCGGCGGC	TTGGAGAGTA	TGTTCTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGCTG	CTGTTTGCGC
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCGG	TCCGTACCTT	CTTGACGAAT
1051	GCCGGACGCG	CGACGTTTCA	CGTTGCCATG	ACTTCGGTCG	GGGTCAATTT
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT	GCTTTCGGGA	GAAACGTTCA
1151	AACCCGTTTA	CGACAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG	CGGGGACGGT	GATTAACCCG	CTCGTGCCGT	GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGGCGT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCTT	GTTATTTCGGC
1351	TGGACGGGGC	TGACTTTGAG	CAAAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

1	MFAFKSLLD	PRGEALAVV	ALIAAMGYT	ISLEWLPHMS	IIAAIVVLIL
51	YGLARGLKYN	DMQAGMIGAL	NOGMGAVYLE	FFIGLMVSAL	MMSGAIPTLM
101	YYFGFLISPT	YFYFSAFALC	SVIGVSISS	LTACATVGVA	FMGMAAFAQA
151	DMAMTAGAIV	SGVFFGDKMS	PLSDTTGISA	SIVGIDLFEL	IKNMMYTTIP
201	AWLISAALML	WLLPSVAAQD	LNSVESFRSQ	LEATGLVHGY	SLIPFALLVV
251	LALMRVNAV	AMLEFTVIAAV	AVTYLHSTPD	LRQLGAWFYG	GKLEGEAFK
301	DIAKLISRG	LESMTFTQTI	VILGMSLGL	LFALGVIPSL	LEAVRTFTLN

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
451 WTGLTSLSK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTTCGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGCAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTCTCTCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTCCGCGT TCCATCGTCG
551 GCATCGACTT GTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTTCG
651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CCGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCGCT GTTGCTCATT
751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTGCGCTG GCTGTAACGT ATCTGCACAG CACGCCCCAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTGCGC
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTCTCGGGT GAAACGTTCA
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCCGGGACG
1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCTT TTTCTGCTAT TTGAGTTTGG CTTGACCCTT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLLDL PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MSGAIPITLM
101 YYGFGILSPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFHE IKNMYYTTIP
201 ARLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRTFLT
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
451 WTGLTSLSK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLLDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLLDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQMGAIYLF FFIGLMVSALMSGAIPTLMYYGFGILSPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLF FFIGLMVSALMSGAIPTLMYYGFGILSPTYFYFSAFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVA FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVA FMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m709.pep	SIVGIDLFHEIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMYYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

a709.seq

1	ATGTTTCGCTT	TCNAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCNCTTGG
51	CGTCGTCGTC	GCTCTGATTG	CCGCGATGGG	CTATACCATC	ATTNNNTTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTNGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAATACAAC	GATATGCAGC	AGGGCATGAT
201	AGGCGCGTTG	AATCAGGGTA	TGGGCGCGAT	TTACCTNTTT	TTCTTCATCG
251	GCGTGATGGT	CAGCGCGCTG	ATGATGAGCG	CGCGCATTTCC	GACGCTGATG
301	TATTACGGTT	TCGGACTGAT	TTCCCCGACT	TATTTTTATT	TTTCCGCTT
351	CGCGCTGTGT	TCCGTTCATCG	GCGTGTCCAT	CGGCAGCAGC	CTGACCACCT
401	GCGCCACTGT	CGGCGTTGGC	TTNATGGGTA	TNNNGNCGGC	GTTTCNGGCC
451	NANATGGNGN	NGNNGNNGGN	CNNGATTGTN	NNGNGNCGAT	TNTTNGGCGN
501	CAAAATGTCN	CGCTTTCCG	ATACGNCGGG	CATNTCCGCG	TCCATTGTGC
551	GTATCGACCT	GTTTGAACAC	ATCAAAAATA	TGATGTACAC	NACCATTCCC
601	GCGTGGCTCA	TCAGTGNNNC	ACTGATGCTG	TNGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GCACTGCTAT	TCGCTGATTG	CGTTTGCGCT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCTATGCTCT	TTACCGTCACT
801	TGCCGCCGTT	CGCGTAACGT	ATCTGCACAG	CACGCCGATG	CTCGCTCAGC
851	TCGGCGCGTG	GTTTTACGGC	GGCTACAAAC	TCGAAGGCCA	AGCGTNTANA
901	GACATTGCCA	AACTCATTTT	TCGCGGCGGT	TTGGAAAGTA	TGTTTTTTCAC
951	GCAGACCATC	GTGATTCCTG	GGATGAGCCT	TGGCGGGCTG	CTGTTTGCAC
1001	TGGGCGCGAT	TCCTTCCCTG	CTGGATGCCG	TCCGCAGCCT	TTTGACGAAT
1051	GCCGGGCGTN	CCACATTACG	CGTTGCCATG	ACTTCGGTCG	GGGTTAATTT
1101	CCTGATCGGC	GAGCAATATT	TGAGTATTTT	GTGTGCTNGT	GAACCGTTCA
1151	AACCTGTTTA	CGATAAGCTC	GGTCTGCATT	CGCGCAATCT	GTCGCGGACG
1201	CTGGAAGATG	CGGGGACGGT	CATCAACCCG	CTCGTACCGT	GGAGCGTATG
1251	CGGCGTGTTT	ATCANCCACG	CGCTGGGCGT	GCCGGTTTGG	GAATATCTGC
1301	CGTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTGACCTT	GTTATTCCGT
1351	TGGACGGGGC	TGACTTTTGG	CAAAAAATAA		

a709.pap

```

1  MFAFXSLLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMOQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLISPT YFYFSAFALC SVIGVSIGSS LTTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFEH IKNNMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRXNAVV AMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGGI LFLGAIPLSL LDVARSFLTN
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSRNLST

```

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	MFAFXSL	DMPRGEALAVV	VALIAAMGYTII	XLEWLP	HMSIIAAI	VVLILYGL	LARG	GLKYN
m709	MFAFKSL	DMPRGEALAVV	VALIAAMGYTII	SLEWLP	HMSIIAAI	VVLILYGL	LARG	GLKYN
a709.pep	DMQQGM	IGALNQGM	GAIIYLFF	FFIGLM	VSALM	MSGAIPT	LMYYGF	GLISPT
m709	DMQQGM	IGALNQGM	GAIIYLFF	FFIGLM	VSALM	MSGAIPT	LMYYGF	GLISPT
a709.pep	SVIGVSI	GSSSLT	TCATVGV	AXMGXXX	AFXAMXXX	XXXXXIV	XXAXGX	KMSPLS
m709	SVIGVSI	GSSSLT	TCATVGV	AFMGMAA	FQADMAM	TAGAI	VS	GAF
a709.pep	SIVGIDL	FEHIKN	MYTTIP	AWLISX	XLMLXL	LP	SVA	AQDL
m709	SIVGIDL	FEHIKN	MYTTIP	AWLISA	ALMLWL	LP	NVA	AQDL
a709.pep	SLIPFALL	VVLALMR	VNAV	VAMLF	TVIAA	VA	VTYL	LHST
m709	SLIPFALL	VILALMR	INAV	VAMLF	TVMVA	VA	VTYL	LHST
a709.pep	DIAKLIS	RGGLES	SMFFTQ	TIVILG	MSLG	LLFAL	GAIP	SLLDA
m709	DVVKLIS	RGGLES	SMFFTQ	TIVILG	MSLG	LLFAL	GVIP	SLLAI
a709.pep	TSVGVNF	LIGE	QYLSIL	LSGET	FKPVYD	DKLGL	HSRNL	SRTLE
m709	TSVGVNF	LIGE	QYLSIL	LSGET	FKPVYD	DKLGL	HSRNL	SRTLE
a709.pep	IXHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GW	TGLT	LSKKX
m709	ISHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GW	TGLT	LSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGA	AACCC	ACGAA	AAAT	CCGCT	GATG	CGCA	AATTGA	ATAA	TGGTC
51	CCAGG	AGGAT	ATGGC	CGGAA	AGCTG	GCGAT	GTCG	CAGGC	GGGT	ATGCCA
101	AAATC	GAACG	GGGCG	AAACG	CAGTT	AAATA	TCCCG	CGTTT	GGAG	CAGTTG
151	GCTCA	GATTT	TCAAA	ATCGA	TATGT	GGGAC	TTGCT	CAAA	CGGG	CGGTGG
201	TGGGA	TGGTG	TTTC	GATTA	ATGA	AGGTGA	TAGTG	GTGGC	GATAT	TGCGT
251	TGTAT	GCGTC	GGGT	GATGT	TCGAT	GAAAA	TAGA	ATTTT	AAAA	TGGAG

```
m710.pep
  1  METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51  AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
101  LKHCKEMLEQ KDKEIELLRK LTETV*
```

```

a710.seq
1  ATGGAACCC  ACGAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGGCAGGC  GGGTATGCCA
101 AAATCGAACG  AGGCGAAACG  CAGTTGAATA  TCCCGCGTTT  GGAGCAGGTT
151 GCGCAGATTT  TCAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGCGCGCGG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATAT
301 GAATTAAAC  ACTGTAAAGA  ATGTTGGAA  CACAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A

```

```

.a710.pep
      1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
     51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
    101  ELKHCKEMLE HKDKIEILLR KLTETV*

```

```

                                10      20      30      40      50      60
a710.pep    METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
              |||||
m710        METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
              10      20      30      40      50      60

                                70      80      90     100     110     120
a710.pep    LLKSGGGGMVLQINDVDTSNGEFAYTAQDASGKAGFVKMKELKHCKEMLEHKDKKEIELLR
              |||||:::||:||||:|:| | :|||::|||:|||||
m710        LLKSGGGGMVFAQINEGD SG-GDIALYASGDVSMKIEFLKMELKHCKEMLEOKDKKEIELLR
              70      80      90     100     110

```

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTGGC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTREAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFQYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGM
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```
1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTDD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFETS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

a711/m711 99.8% identity in 431 aa overlap

	10	20	30	40	50	60
a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTDD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTDD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFETSFKQLEKEFYEKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFETSFKQLEKEFYEKQRLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430

1149

a711.pep

AKFMAKKKVLKX

|||||||

m711

AKFMAKKKVLKX

430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTGTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGTTGTCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGCGTGCCA AAAATGCCGA CATTGCCACG GCCTTGTCCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTAATCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCGCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNLGH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAACAA CCCCCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSECE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKWVKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVWLQPLR
301 VHVIDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSDFD VIGRLGPEAA
51 IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
m713	10	20	30	40	50	60
a713.pep	70	80	90	100	110	120
m713	70	80	90	100	110	120
a713.pep	130	140	150	160	170	180
m713	130	140	150	160	170	180
a713.pep	190	200	210	220	230	240
m713	190	200	210	220	230	240
a713.pep	250	260	270	280	290	300
m713	250	260	270	280	290	300
a713.pep	310	320	330	340	350	360
m713	310	320	330	340	350	360
a713.pep	370	380				
m713	370	380				

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
  51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101  TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151  CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
 201  CCGTACGGGC AAAAACCGCC AGCACCGTGT GTTGGCCGTC ATGGCCAAGC
 251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351  TGTAACCGCG GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551  CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
  51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
 101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
 151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
  51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101  TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151  AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
 201  CCGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGGCCGTC ATGGCCAAGC
 251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351  TGTAACCGCG GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551  CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
  51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
 101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
 151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

a714.pep	10	20	30	40	50	60
m714	10	20	30	40	50	60
a714.pep	70	80	90	100	110	120
m714	70	80	90	100	110	120
a714.pep	130	140	150	160	170	180
m714	130	140	150	160	170	180

```
MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPSSAGQMLADW
|||||
MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPRSAGQMLADW
|||||
ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR
|||||
ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR
|||||
AGDRLAPQEIIMVWHVNVVRGGNNRITRFRAAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
|||||
```

1154

m714 AGDRLAPQEIIMVWVHVNRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq

```

1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep

```

1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
	: : : : :					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGSAGSAGSAGSAGSAGS					
	10	20	30	40	50	60
	60 70 80 90 100					
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	: : : : : :					
g716	SCGAAASKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq

```

1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep

```

1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	: : : : :					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70 80 90 100					
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	: : : : :					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAC  CCTGTTCCCTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCGTCTCTGA  CCGCCGTGTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CCGCGCGCCGT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCTG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGCATT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCCCT  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgctGTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGCTTGG  CCGTACCCTG  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCCCTG  TGCCGCTCA  TTCTGCTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCCG  TTTATATGCA
1251  CACATTGTTT  TGCTTgGCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPILLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLFSAATA ALLSRPSPLP
101  SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLRMGRAL AFSSAQLVPK
151  LAILLLLPLT VGLLHFPANT SVLTAVYALA NLAAAAFLF QNRCRLKAVR
201  RAFFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKKY AGLEQLGVYS
251  MGISFGGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAAALLAS
301  ALCLTGIFSP LASILLPENY AAVRFTVWSC MLPPLFYTLT EISGIGLNVV
351  RKTRPIALAT LGALAANLLL LGLAVPSGGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAAAYLAG
451  CILRHRKLNH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCCGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAC  CCTGTTCCCTG  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGTA  CCGCCGTGTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCTG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGCATT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGCTTGG  CCGTGCCTGC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCCTG  TGCCGCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCCG  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```


This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMOTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFTKTLF PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLEPIRFL LVLMEGRAL AFSSAQLVPK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*
```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMOTAAGLTVSVLCLGLDQA						
g717	10	20	30	40	50	60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMOTAAGLTVSVLCLGLDQA						
m717.pep	70	80	90	100	110	120
YVREYYATADKDTLFTKTLFPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE						
g717	70	80	90	100	110	120
YVREYYAADKDTLFTKTLFPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE						
m717.pep	130	140	150	160	170	180
LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTAVLTAVYALA						
g717	130	140	150	160	170	180
LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTSVLTAVALA						
m717.pep	190	200	210	220	230	240
NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY						
g717	190	200	210	220	230	240
NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPLALSSIAWGLASADRLFLKKY						
m717.pep	250	260	270	280	290	300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS						
g717	250	260	270	280	290	300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS						
m717.pep	310	320	330	340	350	360
ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAISGIGLNVVRKTRPIALAT						
g717	310	320	330	340	350	360
ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT						
m717.pep	370	380	390	400	410	420
LGALANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF						
g717	370	380	390	400	410	420
LGALANLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF						
m717.pep	430	440	450	460	470	
CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX						
g717	430	440	450	460	470	
CLASSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKNLHKLHLYLKKQGFPLX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTTG CCGCCGCTGC
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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGCTTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTCCAAA GCATCTTTTC
801 AACGCTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCGCG
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTC GGTATTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCGTCTGCTG CTGGGGCTTG CCGTACCGTC CGCGGCGCGG CGCGGCGCGG
1151 CGGTTGCCCTG TGCCGCCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151 LAIIIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPLFLCTLV EISGIGLNVV
351 RKTRPIALAT LGALAAANLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLGA
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

```

a717.pep      10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
|||||
m717          10      20      30      40      50      60
MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA

a717.pep      70      80      90      100     110     120
YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF
|||||:|||||
m717          70      80      90      100     110     120
YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF

a717.pep     130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA
|||||
m717         130     140     150     160     170     180
LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA

a717.pep     190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
|||||:|||||
m717         190     200     210     220     230     240
NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY

a717.pep     250     260     270     280     290     300
AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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1159

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250       260       270       280       290       300
           310       320       330       340       350       360
a717.pep  ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||:|||||
m717      ALCLTGIFSPLASLLL PENYA AAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310       320       330       340       350       360
           370       380       390       400       410       420
a717.pep  LGALAANLLLLGLAVPSGGARGA AVACA ASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||:|||||
m717      LGALAANLLLLGLAVPSGGARGA AVACA ASFWLFFFAFKTESSCRLWQPLKRLPLYLHTLF
           370       380       390       400       410       420
           430       440       450       460       470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           ||:|||||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           430       440       450       460       470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCCGCA CGCTTTCCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTC AAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCGCGGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQRNG LFRTLWLYM FKHYAVHDFE EFLEYGMPI RIGKYGAGT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVQ
251 IPESWVRDKL VIPDVQEGEA VLVROVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILQDTHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CCGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACAG CGGCAGGCAT
801 CATGCCAGAA GGTATGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCGCTG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCGGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGAGC GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```
1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHLEFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTRPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNR ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*
```

a718/m718 98.4% identity in 380 aa overlap

```
120 130 140 150 160 170
a718.pep DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS DGLYLPRNFIHRPQSWFKWDKDNGLLLRT
m718 |||||:|||||
SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT
10 20 30

180 190 200 210 220 230
a718.pep RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
m718 |||||:|||||
RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
40 50 60 70 80 90

240 250 260 270 280 290
a718.pep RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLOMADW
m718 |||||:|||||
RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADW
```

1161

	100	110	120	130	140	150
	300	310	320	330	340	350
a718.pep	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
	160	170	180	190	200	210
	360	370	380	390	400	410
a718.pep	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIPIESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIPIESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
	420	430	440	450	460	470
a718.pep	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
	480	490	500	510	520	
a718.pep	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

1	ATGGAGCCGA	TAATGGCAAA	AAAGAACAAT	AAAACATAAA	TCCAAAAGCC
51	CGAAGCTGCA	TTGCAGACGG	ACGTGGCTCA	AATTACGGCG	ACCGGTCGGG
101	TTATCGCCGA	GCATCCGTCC	AATTTTATTA	CGCCGCAAAA	GATGCGGGCC
151	CTCTTCGAGG	ACGCAGAAAG	CGCGGACATC	CGCGCCCAAC	ACGAGCTTTT
201	CGCGGACATT	GAGGAGCGCG	ACAGCGACAT	CGCGGCAAA	ATGGGGACGC
251	GCAAACGCGC	GCTGCTGACG	CTCAACTGCG	GCGTCGCCCC	GCCGCGAAAT
301	GCGACGCCCG	AAGAAGAAAA	GCTGTCCGAC	CAAGCCTACG	AAATGATGGA
351	CAGCCTGCCT	ACCCTCGAAG	ACCTGATTAT	GGATTGTATG	GACGCGGTAG
401	GGCAGCGATT	TTCTGCGTTG	GAGGTCGAGT	GGGTATTTTC	AGACGGCCTT
451	TACCTACCCC	GAAACTTTAT	CCACCGCCCG	CAAAGCTGGT	TCAAATGGGA
501	CAAAGACAAC	GGGCTGCTGC	TGCGTACCCG	CGAAAATCCG	GAAGGCGAAG
551	CGTTGTGGCC	GCTGGGCTGG	GTCGTTTATA	CCCAAAAATC	GCGCAGCGTC
601	CAGCAGGCGC	GCAACGGGCT	TTTCCGCACG	CTTCTCTGGC	TGTATATGTT
651	CAAACTACAC	GCCGTCCACG	ATTTTGCCGA	GTTTTTGAG	CTGTACGGCA
701	TGCCCATCCG	TATCGGCAAA	TACGGCGCGG	GCGCAACCAA	AGAGGAAAAA
751	AACACCTGCG	TTCGAGCGGT	GGCGGAAATC	GGTCACAACG	CGGCAGGCAT
801	CATGCCAGAA	GGTATGGAAG	TAGAGCTCCA	CAACGCGGCA	AACGGTACGA
851	CGGCAACCA	CAATCCGTTT	TTGCAGATGG	CCGACTGGTG	CGAAAAATCG
901	GCGGCGCGGC	TGATTTTGGG	GCAAACGCTG	ACCAGCGGTG	CGGACGGAAA
951	ATCCAGCACC	AACGCGCTGG	GCAATATCCA	CAACGAGGTA	CGCCGCGATT
1001	TGCTGGTGTC	GGACGCAAAA	CAGGTGGCGC	AAACCATCAC	AAGCCAAATC
1051	ATCGGACCGT	TCCTGCAAA	CAACTATCCC	CATGCCGACC	CAAACCGCGT
1101	GCCGAAATTT	GAATTGACA	CGCGCGAGCC	GAAAGACATC	GCGGTCTTTG
1151	CCGACGCTAT	CCCGAAACTG	GTGGATGTCG	GCGTACAAAT	CCCCGAAAGC
1201	TGGGTGCGCG	ACAAACTGGT	CATTCCAGAT	GTGCAGGAGG	GTGAGGCTGT
1251	GTTGGTGCGG	CAGGTACCGG	ACAATCCGGT	AAACAGAACT	GCATTGGCGG
1301	CTTTATCCGC	CCACACCGTA	CCATCTAAGG	CTACGGGCGA	GCATCAGGAA
1351	ATATTGGACG	GCGCGTTGGA	TGACGCGCTG	GTTGAGCCCG	ATTTCATTC
1401	TCAGCTCAAC	CCGATGGTGC	GTCAGGCGGT	TGCCGCACTT	AATGCTTGCA
1451	ACAGCTACGA	GGAGGCAGAT	GCCGCACTGA	ATGCGCTTTA	TCCGAATTTG
1501	GACAAACGCG	AACTGCGTAC	CTATATGCAG	CAGGCCTTGT	TTATCAGCGA
1551	TATTTTGGGA	CAAGACCATG	CCCGCGCCTG	A	

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep

1	MEPIMAKNN	KTKIQKPEAA	LQTDVAQITA	TGRVIAEHPS	NFITPQKMRA
51	LFEDAESGDI	RAQHLEFADI	EERDS DIAAN	MGTRKRALLT	LNWRVAPPRN
101	ATPEEEKLS	DQAYEMMSLP	TLEDLIMDL	DAVGHGFSAL	EVEWVSDGL
151	YLPRNFIHRP	QSWFKWKDN	GLLLRTREN	EGEALWPLG	VVHTQKRSRV
201	QYARNGLFRT	LSWLYMFKHY	AVHDFAEFLE	LYGMPIRIGK	YGAGATKEEK
251	NTLLRAVAEI	GHNAAGIMPE	GMEIELHNAA	NGTTATSNPF	LQMAWCEKS
301	AARLILGQTL	TSGADGKSST	NALGNIHNEV	RRDLLVSDAK	QVAQTITSQI

351 IGFPLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq
 1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
 51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
 101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
 151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
 201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
 251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
 301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
 351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
 401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGCGCTT
 451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
 501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
 551 CGTTTGGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
 601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
 651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
 701 TGCCCATCCG TATCGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
 751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCAACAAC CGGCAGGCAT
 801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
 851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
 901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
 951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
 1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
 1051 ATCGGACCGT TCCTGCAAA TCACTATCCC CATGCCGACC CAAACCGCGT
 1101 CCGGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
 1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
 1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
 1251 GTTGGTGCGG CAGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
 1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGG GCATCAGGAA
 1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTCAATTC
 1401 TCAGCTCAAC CCGATGGTGC GTGAGGCGGT TGCCGCACTT AATGCTTGCA
 1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
 1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
 1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep
 1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
 51 LFEDAESGDI RAQHOLFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
 101 ATPEEKLSD QAYEMMDSL P TLEDLIMDL DAVGHGFSAL EVEWVFSDDL
 151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
 201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
 251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS
 301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
 351 IGFPLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHOLFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSL					
m718-1	RAQHOLFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSL					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
	130	140	150	160	170	180

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVHTQKSRSVQOARNGLFRTLWSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVHTQKSRSVQOARNGLFRTLWSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMA DWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMA DWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRDDLVS DAKQAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDDLVS DAKQAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRPVKFEFDTREPKDIAVFADAIPKLV DVGVIPE SWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRPVKFEFDTREPKDIAVFADAIPKLV DVGVIPE SWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDPNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAV AAL					
m718-1	QVPDPNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAV AAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCCGC	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGCG	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCCGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCGG	CGGTTTGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCTGCG	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TGCTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTCGATT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGCGCG	AACTGCTGCC	TGATTTGCAG	GCAAAACAAG	GTTTGCTGCC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

```

1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTTGC GTTGTGACAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CCGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAOTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSQSLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGPSAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPE GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGVPOYLA APSAQPTDKM LSPFLSTQTA
651 AYQAAIQOQT AAYQAALQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVN RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CGGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTG TTTGATTG GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
601 CGGGCGCGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TCGGATATA TCGGTCATGG TAGATACTGG CATAACCGCT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGCTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCGGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCTGCA AAACCGCCTG AACCAGTTAA

```



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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGGGTGGC AACGGCATT AATCGAGGCG ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCAGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCC CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNKGA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNRRL NRLTAKQVQP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGLLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGGCGGTC ATCAACCAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNRNLRLT AKQVQVPAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESELRRAA
101 GRLNALVA AV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

m720.pep      250      260      270      280      290      300
SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRNLRLTAKQVQPVAQAVRLLSTSSLL
a720          |||||
              GLQNRNLRLTAKQVQPVAQAVRLLSTSSLL
              10      20      30

m720.pep      310      320      330      340      350      360
SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720          |||||
              SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
              40      50      60      70      80      90

m720.pep      370      380      390      400      410      420
QTAESELRRAAGRLNALVA AVINQKPLIVRQAPIDGTIHQIAHEFYGDIA RAAELVRLNP
a720          |||||
              QTAESELRRAAGRLNALVA AVINQKPLIVRQAPIDGTIHQIAHEFYGDIA RAAELVRLNP
              100     110     120     130     140     150

m720.pep      430      440
HHHHPAFIKRGTLVNSYAKX

```

a720

|||||
HIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq

```
1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACCTGGC GGCTCGCAAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA
```

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep

```
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHDTVALLN SSRNQLVVVDY EHQTLYKEKN GQPAPAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAQEQAD KGNELITAAL TSGKLLPAQK EWAKGVLPQK GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq

```
1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCGA
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACCTGGC GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
```

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

a721.pep
1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAE AAAAKMLGMS GEEFVKIKES
351 EGK*

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
m721	10	20	30	40	50	60
a721.pep	70	80	90	100	110	120
m721	70	80	90	100	110	120
a721.pep	130	140	150	160	170	180
m721	130	140	150	160	170	180
a721.pep	190	200	210	220	230	240
m721	190	200	210	220	230	240
a721.pep	250	260	270	280	290	300
m721	250	260	270	280	290	300
a721.pep	310	320	330	340	350	
m721	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

m722.seq
1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCG
351 CGCCGTTATC GGCAGCGGCG GCACGCGCGA AATACCGGCA ATCGCCGACG

```

401 AGCCGGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGTGC CCGGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGCGC GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGTGC CCGGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1   ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC  CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGCGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCATT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTTCAGCAT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCGG GTTTCTGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1   MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
51  FAFGHSTQQV EHVDFVAHAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCCTTTTTTTGCGGTGTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTTCGGGAAAAATCACGCTGGTGGTGTCTGCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+ 120
GACGCGCGCGGAAAGCCCTTTTTAGTGCAGCACACAGCAGGCTCGGCTATGTGCGG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTGATGGCGTAGTTTTTGGGAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTTAGCACTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGAGACCAGTGCAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTGTAGTGCCGTTGCCGCGGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GCGGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCGCTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCGCTTTTGAATGGCCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglIII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGACCGG GTTAAGTACA
401 AACAAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGGCAAT
601  ATATCGTTGC  GCCAGCACCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1  MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
 51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKNLK
101  PGETAIFNHE  GAKIVIKQ GK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNAFL
151  VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201  ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

```

              10      20      30      40      50      60
a724.pep    MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              |||||
m724         MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              10      20      30      40      50      60

              70      80      90     100     110     120
a724.pep    GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
              |||||
m724         GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
              70      80      90     100     110     120

              130     140     150     160     170     180
a724.pep    IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              |||||
m724         IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              130     140     150     160     170     180

              190     200     210     220
a724.pep    GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              |||||
m724         GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              190     200     210     220

```

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1  ATGGTGCGCA  CGGTTAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
 51  GCAAATCCAT  ACGCTGCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101  TTGAGCCTGC  CAGCACCGGC  GGCGTATGCG  GACGTTATCA  GGATACCGCC
151  GAATTTGTGG  TGATGGTGGC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201  GCGGCAAGGC  GGCATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251  GCGCTGTTCC  CCGCTGCTT  GACGCGCAGC  GGCTCGGTTT  TGCCGATAGC
301  CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGGT
351  GCAAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401  ACACCTGCGG  GTTGGAAAT  GACCGCTACC  CCGAACGCAC  CGACAATCCC
451  GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501  GTGGCCTGAT  TTCGAGGGGT  TGGACGGCAA  AATTTACGAC  CCGCAATCCG
551  CCGATGAAAT  ACCTGTAAAC  CTAACCCCTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1  MVRTVKS YNG  EADDLAQI H  TLPVWVTY G  GSKVEPAST G  GVCGRYQDTA
 51  EFVVMVA ARN  LRNEQAQR OG  GIDSREIGS N  DLIRAVRRL L  DGQRLGFADS
101  RGLVPKAV RA  IANHVLVQ NA  AVSIYAVEYA  IRFNTCGLEN  DRYPERTDNF
151  DDPNHIFT KY  QGTLSEP WPD  FEGLDGKIY D  PQSADEIPV N  LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

m726.seq

```

1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

m726.pep

```

1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

a726.seq

```

1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

a726.pep

```

1  MTIYFKNGFY DDTLGSIEPG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVVEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*

```

a726/m726 95.5% identity in 201 aa overlap

```

          10      20      30      40      50      60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          10      20      30      40      50      60

```


1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGEAAAAARFAEQKTATAFRLLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEKVVVEKSARLAVAAGAIIGKRQLEDKLNIT
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEKVVIEKSARLAVAAGAIIGKRQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|:|||||:|||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

```

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPPD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFHGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
m727      YARELELARAEEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDPSRNPTGTF
           70      80      90      100     110
           120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX
           120     130
m727      RLFSPQIIPPNETQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

g728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGGAA TGA TGCCCGCG GGGGATGAAG GCGAACAGTC TTGTGGTTCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCAACAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

g728.pep

```

1  MFKKEKPVLL SFFALVEAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLOSEK DYLA LAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEA FVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQ AOVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

m728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATCGG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
	: : : : :					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGKEV					
	: : : : :					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
	: : : : :					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
	: : : : :					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	: : : : :					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	: : : : :					

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310          320          330          340          350          360
m728.pep  YAEAAARRSGGRRDLSHX
           |||||
g728      YAEAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAG
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAAG TCTATTGGAG TTTGCACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLERNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLVRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

a728 / m728    96.3% identity in 377 aa overlap

           10          20          30          40          50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10          20          30          40          50          60

           60          70          80          90          100         110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70          80          90          100         110         120

           120         130         140         150         160         170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLVRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:|||||
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLVRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130         140         150         160         170         180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGVSVDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGVSVDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNLNF					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSFYYLKNLNF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGRRDL SHX					
m728	YAEAAARRSGRRDL SHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA  CATTGAAAC  TACCTTGACC  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCTCAATA  CGAGCAGCCC  AAAGTCGAAG
101  TTGCGGAAAC  CTTCCAAAAC  GACACATCGG  TTTCTTCCAT  CCGCGCGGTT
151  GATTTGGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201  CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACAGCC  GTATTGAACA
251  GCGAAATCTA  CCGCAAACAA  TACATGATCG  AGCGCAACAA  CCTCTGCCCC
301  ACGCTTGCCG  CCAATGCGAA  CGGCTCGCGC  CAAGGCAGCT  TGAGCGGCgg
351  caaTGTCAGC  AGCAGCTACA  ATGTCGGAAT  GGGTGcGGca  tCTTACGAAC
401  TCGATCTGTT  CgGGCGCGTG  CGCagcaacA  GcgaagcAGC  ACTGcaggGC
451  tATTTTGCCA  GCGTTGCCAA  CcgCGATGCG  GCACATTTGa  ttCtGATTGC
501  CACCGTTGCC  AAAGCCTATT  TCAAcgaGcG  TTATGCCGAA  AAAGcgatgT
551  CTTTGCGCGCa  gcGTGTCTTG  AAAACGCGCG  AGGAAACCTA  CAAGCTGTCC
601  GAATTGCGGT  ACAAGGCAGG  CGTGATTTCC  GCCGTGCCCC  TGCGCCAGCA
651  GGAAGCCTTG  ATTGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCa
701  gcCGCGAACA  GGCGCGCAAT  GCCTTGCGAA  CCTTGATTAA  ccGTCCGATA
751  CCCGAagaCC  TGCCCGCCGG  TTTGCCGTTG  GACAagcAGT  TTTTGTGTGA
801  AAAACTGCCT  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGACA
851  TCCGCGCCGC  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901  gcgCGCGCCg  ccTTTTTCCC  GTCCATCCGC  CTGACCGGAA  GCGTCGGTAC
951  GGGTTCTGTC  GAATTGGGCG  GGCTGTTCAA  AAGCGGCACG  GGCGTTGGG
1001  CGTTCGCTCC  GTCTATTACC  CTGCCGATTT  TTAATTGGGG  AACGAACAAG
1051  GCGAACCTTG  ATGTGGCAAA  ACTGCGCCAA  CAGGCACAAA  TTGTTGCCTA
1101  TGAATCCGCC  GTCCAATCCG  CCTTTCAAGA  CGTGGCAAAC  GCATTGGCGG
1151  CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAAGCCGC
1201  GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGA  CTGCGTTACA  AACACGGCGT
1251  ATCCGGCGCG  CTCGATTTGC  TCGATGCGGA  ACGCATCAGC  TATTGGGCGG
1301  AAGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTGCCGAT
1351  TTGTACAAGG  CGCTCgacGG  CGGATTGAAA  CGGGATACCC  AAACCGGCAA
1401  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFQN  DTSVSSIRAV
51  DLGWHDYFAD  PRLQKLIDIA  LERNLSLRTA  VLNSEIYRKQ  YMIERNLLP
101  TLAANANGSR  QGSLSGGNVS  SSYNVGLGAA  SYELDLFGRV  RSNSEAALQG
151  YFASVANRDA  AHLILIAIVA  KAYFNERYAE  KAMSLAQRVL  KTREETYKLS

```

m729.seq

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

m729.pgp

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

          10      20      30      40      50      60
m729.pep  MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
          10      20      30      40      50      60
g729      MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
          10      20      30      40      50      60

```

1179

m729.pep	70	80	90	100	110	120
	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
g729	70	80	90	100	110	120
	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS					
m729.pep	130	140	150	160	170	180
	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	130	140	150	160	170	180
	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAAHLLIATVAKAYFNERYAE					
m729.pep	190	200	210	220	230	240
	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
g729	190	200	210	220	230	240
	KAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAAARSREQARN					
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	250	260	270	280	290	300
	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	310	320	330	340	350	360
	ARAAFFPSIRLTGSGVTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
g729	370	380	390	400	410	420
	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729.pep	430	440	450	460		
	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	430	440	450	460		
	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTCGC
51	ATTATCCGCC	TGCACCATGA	TTCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACGCCCG	ACAGCGGCAT	CCGTGCGGTC
151	GATTTGGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	GCGTACCGCC	GTATTGAACA
251	GCGAAATCTA	CCGCAAAACA	TACATGATTG	AGCGCAACAA	CCTCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTGCGCA	GCACCGCCAA	CCGCGATGCG	GCACATTGTA	GCCTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTATGCCGAA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTC	GCCGTCGCCC	TACGTCAGCA
651	GGAAGCCCTA	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGCGAA	CCCTGATTAA	CCAACCGATA
751	CCCGACGACC	TGCCCGCCGG	TTTGCCGTTG	GACAAGCAGT	TTTTTGTGTA
801	GAAGCTGCCG	GCCGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCCG	CCTTTTTC	ATCCATCCGC	CTGACCGGAA	GCGTCGATAC
951	GCATTCTGCC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACC	GGCGTTTGGT
1001	TGTTTCGACC	TTCCATTACC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG

```
1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```
a729.pep
1  MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNDSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEAAALQ
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*
```

a729 / m729 98.1% identity in 467 aa overlap

```

      10      20      30      40      50      60
a729.pep  MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          |||
m729      MDTTLKTTLT SVAAAFALSA CTMIPQYEOP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          |||
      70      80      90     100     110     120
a729.pep  PRLQKLIDIA LERNDSLRTA VLNSEIYRKQ YMIERNLLP TLAANANDSR QGSLSGGNVS
          |||
m729      PRLQKLIDIA LERNDSLRTA VLNSEIYRKQ YMIERNLLP TLAANANDSR QGSLSGGNVS
          |||
      130     140     150     160     170     180
a729.pep  SSKVGLGAAS YELDLFGRV RSSSEAAALQGY FASTANRDA AHLSLIATVA KAYFNERYAE
          |||
m729      SSKVGLGAAS YELDLFGRV RSSSEAAALQGY FASTANRDA AHLSLIATVA KAYFNERYAE
          |||
      190     200     210     220     230     240
a729.pep  EAMSLAQRVL KTREETYKL SELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          |||
m729      EAMSLAQRVL KTREETYKL SELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN
          |||
      250     260     270     280     290     300
a729.pep  ALATLINQPI PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
          |||
m729      ALATLINQPI PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
          |||
      310     320     330     340     350     360
a729.pep  ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ
          |||
m729      ARAAFFPSIR LTGTGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK ANLDVAKLRQ
          |||
      370     380     390     400     410     420
a729.pep  QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
          |||
m729      QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR ASKEALRLVG LRYKHGVSGA
          |||
```


	430	440	450	460
a729.pep	LDLLDAERSSSYSAEGAALSAQLTRAENLADLYKALGGGLKRD	TQTDKX		
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRD	TQTDKX		
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGTTCGA CTCATACAGC CCGCCCTCGC GCGGGAATTG GCGCAAGACC
101 CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGaCCC GCGCGGCAGC GTTCCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCGGC AATCCAAGGC AATCTTGTTT ACACCGTCCG CTTTTCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCGGAAG
451 GCGGCAATT ACCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCAACGGC GTCGCCCGCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TGCGCAACAT
801 CGCCCCCTTA CCCGCGGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GCGGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAAACCCGT TACCGCCCGA TACGGCAATC CGTATCAAGA AACCCTTAC
1201 ATTGAAGTTT CAGACGGCAT CCGCAACAGC CAAACCCCTGA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAAA ACCGCTCAAA GCCTACAATC TGACCGTTGC
1401 GATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCCTAAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTTCGG AAGGAAAGCA ATATTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1   VKPLRRLTNL LAACAVAAVA LIQPALAADL AODPFITDNT QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGH LLIQQAIIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADANRK MFEHNAKLDR WGNSEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTDAGY KAIAHIQAGD RVLKDEASG ETGYKPVTA YGNFYQETVY
401 IEVSDGIGNS QTLISNRIHP FYSKGWIKI EDLKAGSRL SESGKTQTVR
451 NIVVKPKPLK AYNLTVDWH TYFVKGNQAE TEGVWVHND PPKPKPTNHA
501 QORKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTPD
551 GRQVTQFKNS KANTSKRVKN GKWTFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1   GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGGCGCCGA CTCATACAGC CCGCCCTCGC GCGGGAATTG GCGCAAGACC

```

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GCGCGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCGGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAA AGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQORIS DNYSNLGSNF
201 SDRADANRKM MFEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90     100     110     120
g730.pep  VSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90     100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQORIFDNYNLSNFSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQORISDNYSNLGSNFSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI
          190     200     210     220     230     240

```

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAPGKAAVSGDFSYSYCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAKAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

a730.seq

1	GTGAAACCGC	TGCGAAGACT	CATCAAGCTC	CTTGCCGCCT	GTGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC
101	CGTTTCATTAC	CGATAACGCC	CAACGGCAGC	ACTACGAACC	CGGAGGCAAA
151	TACCACCTCT	TCGGCGACCC	GCGCGGCAGC	GTCTCCGACC	GCACCGGTCA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCG	GATGGGCAAC	CTGCTCATCC
251	AGCAGGCAAA	CATCAACGGC	ACAATCGGCT	ACCACACCCG	CTTTTCCGGA
301	CACGGATACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCCGCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAACC	TACGGGTGCA	CGCGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCACGCA	GCATCAAAC	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTC
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTTCGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TATCAACGGC	GTCCGCCCGC
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCAA	TGCGCAACAT
801	CGCCCCCTTG	CCCGCCGAGG	GCAAATTTCG	CGTCATCGGC	GGCTTGGGCA
851	GCGTGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGGAAG
1001	CTGCGGTTAG	CGGGGATTTT	TCTGCTGCAT	ACAATACAAG	AACAACCTAGA
1051	AAAGTTACTA	CAGAAACAGA	GGGGTTAAAT	AGAATCAGAC	AGAACCAGAA
1101	AAATAGTAAT	ATACATGAGA	AAAATTATGG	AAGAGATAAT	CCTAATCATA
1151	TTAATGTTTT	ATCTGGAAAT	TCTATACAAC	ATATACTGTA	TGGAGATGAA
1201	GCAGGAGGTG	GGCATCTTTT	TCCTGGCAAA	CCTGGTAAGA	CAACATTCCC
1251	CCAACATTGG	TCAGCCAGTA	AAATAACTCA	TGAAATTAGT	GATATCGTTA
1301	CATCCCCAAA	AACGCAATGG	TATGCACAGA	CTGGAACAGG	CGGCAATAT
1351	ATTGCTAAAG	GAAGACCAGC	TAGGTGGGTA	TCATATGAAA	CGAGAGATGG
1401	AATTCGTATC	AGAACAGTTT	ATGAACCTGC	AACAGGAAAA	GTGGTAACCTG
1451	CATTCCCCGA	TAGAACCTCT	AATCCCAAAT	ATAACCCTGT	AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

a730.pep

1	VKPLRLRIKL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGQINV	IQDYTHRMGN	LLIQANING	TIGYHTRFSG
101	HGYEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGP
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGSNF
201	SDRADEANRK	MFEHNAKLDR	WGNMSEFING	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAVIG	GLGSVAGFEK	NTREAVDRWI
301	QENPNAAETV	EALVNVLPFA	KVKNLTAAK	PGKAAVSGDF	SAAYNTRTTR
351	KVTTETEGLN	RIRONQKNSN	IHEKNYGRDN	PNHINVLSGN	SIQHILYGD
401	AGGGHLFPK	PGKTTFPQHW	SASKITHEIS	DIVTSPKTQW	YAQTGTGGKY
451	IAKGRPARWV	SYETRDGIRI	RTVYEPATGK	VVTAFPDRTS	NPKYNPVK*

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAANKVAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRONQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGDEAGGGHLFPKPGKTTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRKKTGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag  cgtttttcatG  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTCCGAA  ACGGAACCGA  GTGGCACCAG  AAAGGCGGCG  AAGCCTTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG  LSVRVRLDGR  GKIALRLDGR  RAVLSSDVAA  SGERYTAEHG
51  LFGNGTEWHQ  KGGEAFFGFT  DAYGNSVETS  CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGCGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCCATTTC  GACAGCGGCA  AAGTCGCGTT
201 GCGGCTGGAC  GGCAGGCGTG  CCGTCCTCTC  TTCCGACGTT  GCCGCATCCG

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1185

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep				10	20	30
				DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR					
	20	30	40	50	60	70
g731.pep		40	50	60	70	80
		RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731	RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX					
	80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGG
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTT GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTAD	DFRAFSCENGLSVHVRRL			
m731		MNIRFFALTVPVL	SLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHL				
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE					
m731		DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE					
		70	80	90	100	110	120

a731.pep TSCRARX
 m731 TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtC CTGCCGGTGC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTACAG ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtattGG TcaaTTCGGG
951 TTCggcttCC GCGTCGGAGA TTGtgcCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTGAGG ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 TCGGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGCG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732 . pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGF A EKDGRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEGGLGME IGQEDGFVKV VSPIEDTAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDG M VLKAVPEDYV YGMGGDPLAG
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732 . seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTACAG ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCATTCTCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

```

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGCGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTALYYTPT NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
	10	20	30	40	50	60
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSSEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSSEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDMVLKAVPEDYVYGMGGDFLAG					
	250	260	270	280	290	300
m732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
	310	320	330	340	350	360

1188

	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGI	VPDVEVKDKERIFESREADL	VGHIGNPLGGEDVN	GETLAV		
g732	KLTTALYYTPNDRSIQAQGI	VPDVEVKDKERTFESREADL	VGHIGNPLGGEDVN	SETLAV		
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKK	DEDLSSRRIPNPAKDDQLR	KALDLVKSPEQWQKSLGL	AACK		
g732	PLEKDADKPAVKEKGKKKK	DEDLSSRRIPNPAKDDQLR	KALDLVKSPEQWQKSLGL	AACK		
	430	440	450	460	470	480
	490					
m732.pep	PVSNKDKKKDKKKX					
g732	PVSNKDKKKDKKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGTTTGTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AATCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGCTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCTG CAGTTCCAAG AGCGGACGGT
651 CGAAAAGGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CCGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATAACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCAGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGGATTTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAC
1251 CCTTGCCGTG CCGCTTGAAG AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGAYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRALI KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLGA
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAACK PVSNKDKKKD KDKK*

```


a732/m732 99.6% identity in 494 aa overlap

a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGGLGMEIGQEDGFVKV
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGGLGMEIGQEDGFVKV
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP
a732.pep	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
m732	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
a732.pep	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
m732	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
a732.pep	PVSNKDKKDKKDKKX
m732	PVSNKDKKDKKDKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGa cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATTTG GGA CTGCTGC

```

1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPCTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	: : : : : :					
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	: : : : : :					
g733	YFAEAANKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq
 1 ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
 51 GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
 101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
 151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTGCAAAG GTCAGGACAC
 201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
 251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCGAAAGC CTTGGGCGCG
 301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
 351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
 401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGCGCGG
 451 GCTGTTTCGCT CCTTAATCCA ACACCTGAAA TAA

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep
 1 MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
 51 KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
 101 MRVENAVVIT SPRFTSVHQQV ALNQCIKKYG AQQCGLQTV YCTSSSYGG
 151 AVRSLIQHLK *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)
 1 TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTCGCT
 51 GAACAATACC TGTGTCGCGC TGGCATAACC GAAAGCCTTG GCGCGCTGC
 101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
 151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
 201 CGGCTTGGA ACAGTGTATT GCACATCTTC TTCTTATTAC GCGGAACTG
 251 TCGCTCTTT GATTCAAAAT CTCAAATAA

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)
 1 SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAV VITSPRFTSVH
 51 QVALNQCIKK YGVQGCGLQ TVYCTSSSY GGTVRSLIQN LK*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVSVLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL		

1192

	40	50	60	70	80	90
m734.pep	40	50	60	70	80	90
	GALRVDNAVVITSPRFTSVHQVALNQCICKYGVQGQCGLETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVITSPRFTSVHQVALNQCICKYGAQGQCGLETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150
m734.pep	LKK					
g734	LKK					
	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTGCACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCTT TTCTGCAAGG GTCAGGACAG
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCGCG TCGGTCTGT
251 CGTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATCGGCTT GGAACAGATG TATTGCAGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCCAAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNFQNDANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDITLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

a734/g734 95.6% identity in 160 aa overlap

```

      10      20      30      40      50      60
a734.pep  MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g734      MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA
          10      20      30      40      50      60

      70      80      90      100     110     120
a734.pep  FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVLAYPKALGAMRVENAVVITSPRFTSVYQV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g734      FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV
          70      80      90      100     110     120

      130     140     150     160
a734.pep  ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g734      ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX
          130     140     150     160

```

```
g735.seq      not found yet
g735.pep      not found yet
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

m735.seq

```
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGCGCGAC GCTGTCTGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCGGTCTGAA ACGGAAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG
```

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51 CCGCCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CCGCTTTTGC GAAGCAGCAG GCGGTCAATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CCGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTTCGCG GCTTCTCTGT TCGCGGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CCGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTTCG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDING
 201 LIKSAAFVVA VTLLIAVHGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCCG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCCTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCCG GTGGTTGCCC CGCGTTTTTG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDING
 201 LIKSAAFVVA VTLLIAVHGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	: : : : :					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	: : : : :					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
	: : : : :					
g736	MKTTGQLEAMNVMVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVSWLGLDS					

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYD	VINGLIKSAAFGVA	VTLIAVHQGFHCV	PTSEGILRASTR	TVVSS	
g736	GIFWPQMNNITIHYD	VINGLIKSAAFGVA	VTLIAVHQGFHCV	PTSEGILRASTR	TVVSS	
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAW	MFTDX				
g736	ALTILAVDFILTAW	MFTDX				
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTCGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCCGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATCAAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCGCCCGA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCCATGC	CGCTTTTGGC	TTTCGATTTT	AACGTGGCGG	GTATTTTCGG
501	CGCGTATTTG	GTCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAAT	GCAGAACAAC	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCGCGTT	CGCGCTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTGGCGGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAGV
151	FSMPLLASIF	NVAGIFGAYL	VGVTWLGLDS	GIFWSQMNN	ITIHYDVI
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRTVVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG	VLSVLIVAVS
m736	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG	VLSVLIVAVS
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV	LAAILFASSA	GGAMTSEIGL
m736	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV	LAAILFASSA	GGAMTSEIGL
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAG	VFSMPLLASI	FNVAGIFGAYL	VGVTWLGLDS
m736	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAG	VFSMPLLASI	FNVAGIFGAYL	VGVTWLGLDS
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNN	ITIHYDVI	GLIKSAAFG	VAVTLIAVHQ	GFHCVPTSEG	ILRASTRTVVSS

1196

```

m736      GIFWSQMONNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240
a736.pep   250      259
           ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq.

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLLSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLLTAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAEKAAWAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

a737.seq
 1 ATGAACCTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
 301 GTGATTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
 1 MNFKRLLLTAAATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
 101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR	
m737	MNIKHLTSAATALLSISAP	ALAHHDGHG	DDDHGHAHQ	HNKQDKIISR	AQAEKAALAR	
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYD	VEIVKNGQY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDLEHDNGRPHYD	VEIVKNGQY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
 1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACCTGCC
 51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCGACT TTTACCACGA TGCCGCCGCG
 151 GCGGCCGCGC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAAA ATCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCCG GCTGGGAAA CACCCCTCTG CTTCAAAACA TCATCGTTCA
 501 CAGAGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCCTCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAAGC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
 951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
 1001 ACACCATAA CGACAACCTT CTCAGCACCT TGTTACCCA TTCCCACAAC
 1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
 1151 CCCCCGCATC ACTTTTCTCG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCGG
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC AACTGACCG CCTCCGCCGC CATATTCGCA
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
 1401 CCCCCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
 1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTAC TCCGCCACCT

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACAA
1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLIFA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYQERIV TLFAWSLLIG SLLOSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGW N SFAQQTFLIN AEQHTIHDNF LSTLFTSHSN
351 IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYIT RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAE EA TLKALKYR PY SATYRIALYL MRQGVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT
101 TCGCGTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGCCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGCGCGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTACAGC CGTGGGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILFTFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIDNLL SNNLFTHSHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

```

      10      20      30      40      50      60
m738.pep MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL
          10      20      30      40      50      60

      70      80      90      100     110     120
m738.pep TAGKKLFDVKIPAISFLLFMAAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      TAGKKLFDVKIPAISFLLFMAAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL
          70      80      90      100     110     120

      130     140     150     160     170     180
m738.pep VAHFGQERIVTFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      VAHYGQERIVTFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN
          130     140     150     160     170     180

      190     200     210     220     230     240
m738.pep NLGHYLMWGI LAAAYLNGQRKIPAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      NLGHYLMWGI LASAYLNGQRKIPAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW
          190     200     210     220     230     240

      250     260     270     280     290     300
m738.pep YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TILFTFTGIR YETAVERVANGGFTDLPRQI
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      YFRSDKSNRR TMLGIAAAVFLTALFQFSMNAILETFTGIR YETAVERVANGGFTDLPRQS
          250     260     270     280     290     300

      310     320     330     340     350     360
m738.pep EWNKALAAFQ SAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNNLFTHSHNIVLQLLAEMG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      EWNKALAAFQ SAPIFGHGWN SFAQQTFLINAEQHTIHDNLFSTLFTSHNIIQLLAEMG
          310     320     330     340     350     360

      370     380     390     400     410     420
m738.pep ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      ISGTLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML
          370     380     390     400     410     420

      430     440     450     460     470     480
m738.pep FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738      FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK

```

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPLSFYADFSLVNFALPEYPETQTWAEATLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

a738.seq

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCCGCGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGCTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCGGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

```

1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLFL TAGKKLFDVK IPPISFLLFA MAAFYQLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYQERIV TFAWSLLIG SLLQSCIIVI
151 QFAGWEDTPL FQNIIVYSQGV VIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAFQ SAPIFGHGWN SFAQOTFLIN AEQNIHDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTYT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVKVAEK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAH	PAAKLP	IIYILPC	FLWIGIV	PFTFALR	LQSPDFYH
m738	MPAETTVSGAH	PAAKLP	IIYILPC	FLWIGIV	PFTFALR	LQSPDFYH
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDV	KIPPI	SFLLF	FAMAA	FWYLQ	ARLMNLI
m738	TAGKKLFDV	KIPPI	SFLLF	FAMAA	FWYLQ	ARLMNLI
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQER	IVTLF	AWSL	LIGS	LLQSC	IVVIOF
m738	VAHYGQER	IVTLF	AWSL	LIGS	LLQSC	IVVIOF
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMW	GILAA	AYLNG	QRKIP	PALGA	ICLIMQ
m738	NLGHYLMW	GILAA	AYLNG	QRKIP	PALGA	ICLIMQ
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSN	RRTIL	GIAAA	VFLTA	LFQFS	MNTILE
m738	YFRSDKSN	RRTIL	GIAAA	VFLTA	LFQFS	MNTILE
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAA	FQSAP	IFGHG	WNSFA	QOTFL	INAEQ
m738	EWRKALAA	FQSAP	IFGHG	WNSFA	QOTFL	INAEQ
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLV	AATLL	TGIAG	LLKR	PLTPA	SFLICT
m738	ISGTLLV	AATLL	TGIAG	LLKR	PLTPA	SFLICT
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAES	DGIAF	KKAAN	LGILT	ASAAI	FAGLLH
m738	FLSPAES	DGIAF	KKAAN	LGILT	ASAAI	FAGLLH
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYI	SANSP	MLSFY	ADFS	LVNFA	LPEY
m738	INELRYI	SANSP	MLSFY	ADFS	LVNFA	LPEY
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQGVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDCKAFAAA	PGHPEA			
m738	MRQGVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDCKAFAAA	PGHPEA			
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCCGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAO PKETPKENHT KPDPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPQADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPHKEILDKLF					
g739	PKNTPAKPHKEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATCAAC CCGAACGCGC ACAA AACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDDAGA Q AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLFX*
  
```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPQHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSPAAPKKNRVKQPQADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPQADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDDAGAQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

```

              190
a739.pep      PKNTPPKPHKEILDNLFX
              |||||:|
m739          PKNTPPKPHKEILDKLF
              180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gTTTGTATT
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTGT CTGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQFDLKRQ TMLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAATCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTGTATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQFDLKRQ TMLFIPIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              |||||
g740           MSRNLLVRLAVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQFDLKRQTMLFIPIILLIVYLFHYFGAFX
              ||| |||||:|||||:|||||
g740           LKQFDLKRQTMFLFIPIVLLVVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTGTATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQFDLKRQ TMLFIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```



```

a740.pep      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||||:|||||||
m740          MSRNLLVRWLVVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep      LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
|||||||:|||||||
m740          LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAA AACTTTCAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAAC TCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QORRGGGGVV AADIGTGLAD ALTAPLDCHKD
51  KGLKSLTLEA SIPQGTITL SAQGAETFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHSA VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACC GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDCHKDKGL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYNGND SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMKVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQNGNKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEGKS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---	ALILTACSSGGGGVAAD	IGAGLADALTAPLDHKDKGLQSLTLDQ		
g741	VNRTTFCCLSLTAGPDS	DRLQRRGGGGVAAD	IGTGLADALTAPLDHKDKGLKSLTLEA		
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAAQGA	EKTY---GNGDS	SLNTGKLKNDKVS	RFDFIRQIEVDGQLITLES	SGE
g741	SIPQNGTLTLSAQGA	EKTFKAGGK	DNLSLNTGKLKNDKIS	RFDFVQKIEVDGQTITLAS	SGE
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTE	QIQDSEHSGKMVA	KRQFRIGDIA	GEHTSFDKLPEGGRAT	YRG
g741	FQIYKQDHS	AVVALRIEKIN	NPDKIDSLIN	QSRFLVSDLGGEHTAF	NQLPDG-KAEYHGK
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYTID	FAAKQNGNGKIEHLK	SPELNVDLAAADIKPD	GKRHAVISGSVLYN	
g741	AFSSDDADGKLTYTID	FAAKQHGKIEHLKT	PEQNVELASAE	LKADEKSHAVILGDTRYG	
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKA	QEVAGSAEVKTVNGIR	HIGLAAKQX		
g741	GEEKGTYRLALFGDRA	QEIAGSATVKIGEKV	HEIGIADKQX		
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTTCT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAGG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCGGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCGGA	GCATTACAGG	AAGATGGTTG	CGAAACGCCA	GTTCAAGATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCCG	TTCAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTCCGCCGCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	GCCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAAQ	GAEKTYGNGD	SLNTGKLKND	KVSRFDFIRQ
101	IEVDGQLITL	ESGEFQVYKQ	SHSALTALQT	EQVQDSEHSG	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAVISGS	VLYNQAEGKS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSKGMVAKRQFRIGDIAGEHTSFDKLPEGGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSKGMVAKRQFRIGDIAGEHTSFDKLPEGGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAKQGHGKIEHLKSPELNVDLAASDIKPDKKRHAIVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAKQGNKGKIEHLKSPELNVDLAADIKPDGKRHAIVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQX					
m741	YSLGIFGGKAQEVAGSAEVTNNGIRHIGLAQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGCGGCG	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTGTACT	GAAAAAACG
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTTCGG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTCGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTCCA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCGGGCG	GGAGCATGAT	TTCTTTGTCT	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACCG	CGATTTGTCT	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCGAC	GGCACCCTCG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAAAA	CGTCAAAGTG	GCAGACGACC	ATGTTCTCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTCGCTGA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTCGGCTA TGTTCCTGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTTCAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
  1 MVYGIAEADA GDSSVLTLLG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
  51 ACNRPLOLPR NTYLGEDWSR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKDLDTG TYGLFGREHD FVVGAYAGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEPDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGRSTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNTNKT HSLTASTREN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDWVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
  1 ATGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
  51 TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCGTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCCGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTGC GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAG TCAACGCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 ACCCGTGCA CATATTCGT TCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
  1 MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN OKTAPFSSTP
 51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDECM SAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFGVYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGE PDGDL S SPLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKT VKV ADDHVPALYN
451 YAKYLNTNKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDNDVDS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFY G EPRTVSMKLD WQF*

```

a742/m742 98.5% identity in 783 aa overlap

```

a742.pep      10      20      30      40      50      60
MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENOKTAPFSSTPACNRPLQLPR
|||||
m742          10      20      30      40      50      60
MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENOKTAPFSSTPACNRPLQLPR

a742.pep      70      80      90     100     110     120
NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL
|||||
m742          70      80      90     100     110     120
NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL

a742.pep     130     140     150     160     170     180
SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR
| |||||
m742         130     140     150     160     170     180
SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR

a742.pep     190     200     210     220     230     240
SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP

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1210

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|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240
          250      260      270      280      290      300
a742.pep  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300
          310      320      330      340      350      360
a742.pep  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360
          370      380      390      400      410      420
a742.pep  RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNP
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECR NAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNP
          370      380      390      400      410      420
          430      440      450      460      470      480
a742.pep  GTPAFTGFSGTVPVWKT VKVADHDHPALYNYAKYLNTNKTSLTAGTRFNVTGRHLHLLGG
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      GTPAFTGFSGTVPVWKT VKVADHDHPALYNYAKYLNTNKTSLTAGTRFNVTGRHLHLLGG
          430      440      450      460      470      480
          490      500      510      520      530      540
a742.pep  LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540
          550      560      570      580      590      600
a742.pep  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          550      560      570      580      590      600
          610      620      630      640      650      660
a742.pep  TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660
          670      680      690      700      710      720
a742.pep  AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720
          730      740      750      760      770      780
a742.pep  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780
a742.pep  WQFX
          ||||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
pseudobactin uptake protein [*Pseudomonas putida*] Length = 819

Score = 152 bits (381), Expect = 6e-36

Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNNTKTHSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494
+T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQFASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
+NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGFELEGRLNANIALYMKVRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
S + + ++G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTGGGVNWNNSKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TGACCGTCAA TGTGTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTTCGATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
551 TGATCCGTAA GTGA

```

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

```

1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG
151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

```

```
351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGCGCAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA
```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```
a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR
```

a743/m743 98.9% identity in 187 aa overlap

```
              10      20      30      40      50      60
a743.pep      MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
              |||||||
m743           MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
              10      20      30      40      50      60

              70      80      90     100     110     120
a743.pep      IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL
              |||||||
m743           IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL
              70      80      90     100     110     120

              130     140     150     160     170     180
a743.pep      SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              |||||||
m743           SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              130     140     150     160     170     180

a743.pep      TVNLIRKR
              |||||||
m743           TVNLIRKX
```

g744.seq not found yet
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```
m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAACTG GAAAGACAGC ATATGCTGTT TATTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAATTTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTAA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATGTA
651 TGGGATAGAT ATTAGCCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAGG TCTTGCTAAC GCCATATGGA TGTTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGGGAAGGAT AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAAACTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTAAAC TTCATTATTT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTG AAATTTTTTG AATTTTAAA CGGGAAGAT AGATTTAAAT
```



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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCCTTA AAGATAGAAA TTATGCAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAACTGAA TATTTAATAT TTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKLEFG FVDAANYRRR ENKDLFNRI VKGEYLDEL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKEVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQO ITFTESKFQA NLGFIERKFK
201 DALSQLKLDK NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQOEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FOREYSIYLL
401 GEIKDHLLFY YSQSDYQNF KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLOFLF DLNVIAYLDN PEDETKPIYH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTTA TGCCTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTAAACGGC TGCATTGCAC
351 CAACCTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTISKQKA TLDVILNDYQ DAQFVEADNH
51 ISPIYRGTA DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPLV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCGCCGCCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCTCAGTT CCGATCCTGC CGACAGCAAT
151 CCGCACCAGC AGGCCGGCGA AACGGGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACCGTA GCGCGCCGCG TGGTGCTGAT
351 TAACGACCGG CTGGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

g746.pap

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPQAGETGA	TESQPTANTA	TPDLSNKAEN	GETAADKKPD	LAGEDKPSAA
101	DEISEPENV	GAVLVILNDR	LELDSNIKGE	ESEKLQQAET	AKTEPKQAKT
151	RAAEKVSATA	DSTDTVAVEK	PKRTAEPKPK	KAERTAEAKP	KAKETQTKAEK
201	VADPKPTAAE	KTKPDTAKSD	SAVKEAKKAD	KAEGKKTKAEK	DRSDGKKHET
251	AQKTDRADKT	KTAEKEKSGD	AGKKAIIQAG	YAEKERALSIL	QRKMKAAGID
301	STITEIMTDN	GKVVYRVKSSN	YKNRADAEERD	LNKLRVHGIA	GQVTNE*

m746.seq

1	ATGTCGGAAA	ACAAACAAAA	CGAAGTCTGT	AGCGGTTACG	AACAACCTAA
51	ACGGCGCAAC	CGCCGCGCCG	TGGTAACGGT	AAGTTGCCTG	GTTGCCGCGT
101	CCTGCATCCT	GCTGGCAGCC	TCCCTCAGTT	CCGGCCCTGC	CGAACAGACT
151	GCCGCGGAAA	CAAGCGGCGT	AGAAAAACAA	CGCGCAGGTG	CGGCACAAC
201	CCCTGCCTTG	AAATCCGCGC	CCGACAACCT	GCAGGACTTG	GCAGGCGAAG
251	ACAAGCCTTC	TGCCGCGCAC	AGCGAAATCA	CGCAGCTGTA	AAACGTAGGC
301	CGCCGCGTGG	TGCTGATTAA	AGCGCGCCTC	GAAGACAGCA	ACATCAAAAG
351	TTTGGAAGCA	TCCGAGAAAC	TGCAACAGCG	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGCG	AAAACAACGC	GCTGCCGAAA	AAGTGCCCGC	AACGCGCGAC
451	AGTACGGATA	CGGTAGCGGT	TGAAAAACCG	AAACGCACGT	CGAAACACAA
501	ACCGCAAAAA	GCGGAACGCA	CTGCCAAAGC	CAAGCCCCAA	GCCAAAGAAA
551	CCAAAACCGC	CGAAAAAAGT	GCCGCAAAAC	CGAAAACCTG	CGCCGAAAAA
601	ACCAAACCGG	ATACGGCAAA	ATCCGACAGC	CGGTAAGAG	AGTCGAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	TGCTCCGACG
701	GCAAAAACAA	CGAAACGGCA	CAAAAAACCG	ACAAAGCCGA	CAAGACCAAA
751	ACCGCCGAGA	AGGAAAAATC	CGTAAAAAAA	GCCGCCATT	AGGCAGGTTA
801	TGCCGAAAAA	GAACGCGCCT	TAGCCCTCCA	CGCAAAATG	AAGGCGCGCG
851	GTATCGATT	GACCATCACC	GAAATTATGA	CGGACAACGG	CAAAGCTTAC
901	CGCGTCAAT	CAAGCAACTA	TAAAAACGCA	AGGATGCGC	AATCGCGATT
951	GAACAAAATT	CGCGTACACG	GTATCGCCGG	TACGGTAAGT	AATGAATAG

m746.pgp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVENK	AAGAAQT PAL	KSAADKPQDL	AGEDKPSAAD	SEISEPENVG
101	APLVLINERL	EDSNIKGLEA	SEKLQQAETA	KTAPKQAKQR	AAEKVPATAD
151	STDTVAVEKP	KRTAETKPKQ	AERTAKAKPK	AKETKTAEVK	ADKPKTAAEK
201	TKPDTAKSDS	AVKEAKKADK	AESKKTAEKD	RSDGKKHETA	QKTDKADKTK
251	TAEKEKSGKK	AAIQAGYAEK	ERALS LRQKM	KAAGIDSTIT	EIMTDNGKVY
301	RVKSSNYKNA	RDAERDLNKL	RVHGIAQGVF	NF*	

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```
m746.pep      10          20          30          40          50
MSENKQNEVLVSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
|||||::||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
g746          MSENKQNEVLVSGYEQLKRRNRRLVTASSLVAAACILLAAALSSDPADSNPAPQAGETGA
              10          20          30          40          50          60

m746.pep      60          70          80          90         100         109
VENKAAGAAQTPLAKSAA-----DKPQDLAGEDKPASAADSEISEPENVGAPLVLINER
:|::|:||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
g746          TESQTANTAQTPLAKSAENGETAADKPQDLAGEDKPASAADSEISEPENVGAPLVLINDR
              70          80          90         100         110         12
```

1215

```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPO
      |||||
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPO
      130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
      |||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
      190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRMKAAGID
      |||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRMKAAGID
      250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCGCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGT CCGGCCCTGC CGAACAGACT
151 GCGGCGGAAA CAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCCTT AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGCG AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAGAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAAGCGGA CAAGACCAAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAGAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKLEA SEKLQQAETA KTA PKQAKQ AAEKVPATAD
151 STDTVAVEKP KRTAETKPK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      |||||
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      10      20      30      40      50      60

```

1216

```

      70      80      90      100      110      120
a746.pep  AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||
m746      AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          |||

      130      140      150      160      170      180
a746.pep  SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQKAERTAKAKPK
          |||
m746      SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQKAERTAKAKPK
          |||

      190      200      210      220      230      240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||

      250      260      270      280      290      300
a746.pep  QKTDKADKTKTAEKEKSGKKAQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
          |||
m746      QKTDKADKTKTAEKEKSGKKAQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY
          |||

      310      320      330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIYKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```
          10      20      30      40      50      60
a747.pep  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
          |||||
m747      LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
          10      20      30      40      50      60
```

```
          70      80      90     100
a747.pep  HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
          ||| |||||
m747      HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
          70      80      90     100
```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272
Score = 59.3 bits (141), Expect = 6e-09
Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR 60
+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
+T + E + GD + ++ EYK RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```
1 ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTAT TCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCGCGAT CGAGTTTCTC
301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAATCTGC GCCTTACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAAACA CACCGCCCAA
601 ACCGCCGTC TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCCAAGGT TTCCGATCCC AAAACCGCGC ACGAGGTTT ATGGACGGGC
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCC CCAAAGACCC
951 CGAGGGTGAT ATCACGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCCGCC CGCCTACAGC
1051 TATTCTCGCG GACCCGCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAATC TTGCGACGG TTTATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```
1 MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKOGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPRQAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGEYQDGD DKLPASAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLOEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
```

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```
1   ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACGCTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTT CCGACGCTGA CCGCCCGCAT CGAGTTCTCT
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCGGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTAGGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGGCCCA AAGACAGCCA TATACGCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACCGCC TCTTCCGCCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGAAAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

```
1   MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DKLPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETCQAA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQTD IFGRRKYSKA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EYIISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

m748.pep	10	20	30	40	50	60
	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
g748	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
	10	20	30	40	50	60
m748.pep	70	80	90	100	110	120
	AGIVTPQQA	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLPAGSGI
g748	AGIVTPRQA	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLPAGSGI
	70	80	90	100	110	120
m748.pep	130	140	150	160	170	180
	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	KPIHLQEMRD	FSNDKLQKSW	CDGDLQLQIC
g748	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	KTVHLQEMRD	FPNDKLQKSW	CDGDLQLQIC
	130	140	150	160	170	180
m748.pep	190	200	210	220	230	240
	AFTPETCQA	LRDIIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP

a748.seq

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAAA
51	CGCAGTCGCA	GCTGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACGGGG	GCAAACCCGC	GAAACGACCG	CGGAAAGCCA	ACACTCGCCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	GCAGGCACTC	TATCGCCGCA
201	CGAGGGCGTT	TGCATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	TAACATTGTC	CGCACCGCTA	CGGCCCGCAT	CGAGTTTCTC
301	ACCCAAGGCG	GCGAATACCA	AGACGGCGAC	GACAAACTTC	CGCCAGCCGG
351	CAGCGCGCAT	TTGGGCAAA	CCTTCAACCC	CGACGGGTTG	ACCGTTACCG
401	TGGGGGTGG	CAGCAGCCTG	TTTGACGGCC	GGTTCGGACT	CAAAAGACAA
451	AAACCGATT	ATTTCGAGGA	AATGCGCGAC	TCTCCAACA	ATAAGCTGCA
501	AAAAAGCTTG	TGCGACGGCG	ATTTGAGCCT	GCAAATCTGT	GCCTTCACCC
551	CCGAACCTCG	CCAAGCCGCC	CTTGCGCACA	TCATCAACA	CACCGCTCAA
601	ACCGCCGTTA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGCGAC	GGCACGGGCA
701	ATCCCAAAAT	TTCCGACCCC	AAAACCTCGC	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCCTCGA	GCAACGGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTTGG	GACAGACGCG
851	CGCTTCAAGA	GCAAACCGAC	ATTTTCGGCG	GGCGCAATA	CAGCGCGCGC
901	CCGATGGAGC	GCAAAAAAGA	AGCCGACCAA	CCGGATTTTT	CCAAAGACCC
951	CGAGGGGAAT	ACCACGCCCA	AAGACAGCCA	TATACGCGTG	GCGAATTCGC
1001	GCGATTCCGA	GTTCTCTAAA	AAACACCCGC	TCTTCGCGCG	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTGC	GGTGTGTGTT
1101	CGTCTGCTAT	CAGGCAAAAC	TTGCCGACGG	ATTCACTTTC	TGCGAAAAAC
1151	TCCTCAACGG	CGAAGCGCTG	GAAGAATACA	TCAGCCCTTT	CGGCGGCGGC
1201	TATTTCCTTC	GTTTGCCCGG	CGTGGAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GTATAA			

a748.pgp

1	MSKNQPAQPI	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHSP
51	QAYPCXGEHG	AGIVTPQQAF	SGKAFPDVTA	QSAQOLENLF	RFLTARIEFL
101	TGGEGYQDGD	DKLPAPGSGI	LICAEFNDTL	TVTGVGSSSL	FDGRFGLKDK
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQDA	LRDI IKHTVQ
201	TAVIRWSIDJ	WQPKSEPGAM	AARNLLHFEV	GTGNPKVSDP	KTAADEVLTWG
251	VAANSLSDEP	WAKNGSYQAV	RLRIHRGFVD	DRTELQEQTD	IFGRRKYSGA
301	PMDGKKEADQ	PDFAKDPEGN	TTPKDSHIRL	ANPRDPEFLK	KHRLFRRAYS
351	YSRGLASSGQ	LDVGLVFCVY	QANLADGFIF	VQNLLNGEPL	EYISPFGGG
401	YFFVLPGEVK	GGFLGOGLLG	V*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	10	20	30	40	50	60
	MSKNQPAQPTTRTLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSPOAYPCYGEHQ					
m748	MSKKQPAQPTTRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPOAYPCYGEHQ					
	10	20	30	40	50	60
a748.pep	70	80	90	100	110	120
	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGGEYQDGGDKLPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGGEYQDGGDKLPPAGSGI					
	70	80	90	100	110	120
a748.pep	130	140	150	160	170	180
	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
	130	140	150	160	170	180
a748.pep	190	200	210	220	230	240
	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
a748.pep	250	260	270	280	290	300
	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA					
	250	260	270	280	290	300
a748.pep	310	320	330	340	350	360
	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
a748.pep	370	380	390	400	410	420
	LDVGLVFVCYQANLADGFI FVQNLLNGEPL EEEYISPFGGGYFFVLPVGEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLLNGEPL EEEYISPFGGGYFFVLPVGEKGGFLGQGLLG					
	370	380	390	400	410	420
a748.pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAG	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGCCACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAGACCGGT	CGGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC

g749.pap

m749.seq

m749 . per

[illegible]

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNNGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNNGRLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVOGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPOPLADYKAYVOGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAE LFS ELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATR VHYERIEPIAE LFS ELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVK EIAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVG GASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSD FQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLG					
g749	LSD FQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCCGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAACCTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCTGTGTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTGTATG CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNNGRLEWE EILKGMVVVD ERENIAAGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEAD LEKLSQPLA
151 DYKAYVOGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD

```

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	MRKFNLTALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT
m749	MRKFNLTALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT
a749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
m749	VPSGQVVFNIKNNSGRKLEWEILKGVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD	
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD	
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG
m749	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX	
m749	EADRKALQASINALAEDLAQLRGILGLKX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCGTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggGCGGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTTGCAG	CCTGCATTG	ACAAGGCGGC	AACGGTGGGG
301	ACGCTGTTTG	AGCCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTTCCGC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCGG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCCGG	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCAGC
701	GGCAGCCCGT	TTCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

g750.pap

m750.seq

m750.pap

BNSDOCID: <WO 9957280A2.1>

1225

```

g750      GGPAAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
QTREAAKGGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFE
          190      200      210      220      230      240
g750      QKREAAKGGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFE
          190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVRGTNAWKRKQIIVMPAANYIVAGGA
          240      250      260      270      280      290
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVCGTNAWKRKQIIVMPAANYIVAGGA
          250      260      270      280      290      300

m750.pep  300      310      320
RQLIQAAEQLKAAFKKAEPVAAAGKKX
          310      320
g750      RQLIQAAEQLKAAFKKAEPVAAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1  GTGAAACCGC  GTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCGCCTG
51  TTCGCCCGAA  CCTGCCGCCG  AAAAACTGT  ATCCGCCGCA  TCCGCATCTG
101 CCGCCACACT  GACCGTGCCG  ACCGCGCGGG  GCGATGCCGT  TGTGCCGAAG
151 AATCCCGAAC  GCGTCGCCGT  GTACGACTGG  GCGGCGTTGG  ATACGCTGAC
201 CGAATTGGGT  GTGAATGTGG  GCGCAACCAC  CGCGCCGGTG  CGCGTGGATT
251 ATTTGCAGCC  TGCATTGAC  AAGGCGGCAA  CGGTGGGGAC  GCTGTTTCGAG
301 CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTACCGG
351 CCGGCCGGGC  GCGGAAGCGT  ATGAACAGTT  GCGGAAAAAC  GCGACCACCA
401 TAGATCTGAC  GGTGGACAAC  GGCAATATCC  GCACCAGCGG  CGAAAAGCAG
451 ATGGAGACCT  TGGCGCGGAT  TTTCGGCAAG  GAAGCGCGCG  CGGCGGAATT
501 GAAGGCGCAG  ATTGACGCGC  TGTTGCGCCA  AACGCGCGAA  GCCGCCAAAG
551 GCAAAGGACG  CGGGCTGGTG  CTGTCGGTTA  CGGGCAACAA  GGTGTCCGCC
601 TTCGCCACGC  AGTCGCGGTT  GGCAAGTTGG  ATACACGGCG  ACATCGGCCT
651 ACCGCTGTGA  GACGAATCTT  TACGCAACGA  GGGGCACGGG  CAGCCTGTTT
701 CCTTCGAATA  CATCAAAGAG  AAAAACCCCG  ATTGGATTTT  CATCATCGAC
751 CGTACCGCCG  CCATCGGGCA  GGAAGGGCCG  GCGGCTGTCG  AAGTATTGGA
801 TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAAATCATCG
851 TCATGCCTGC  CGCGAACTAC  ATTGTCGCGG  GCGGCTCGCG  GCAGTTGATT
901 CAGCGGGCCG  AGCAGTTGAA  GGAGGCGTTT  GAAAAGGCAG  AACCCTTTG
951 GCGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1  VKPRFYWAAC  AVLLTACSPE  PAAEKTVSAA  SASAATLTVP  TARGDAVVPK
51  NPERVAVYDW  AALDTLTELG  VNVGATTAPV  RVDYLQPAFD  KAATVGTLFE
101 PDYEALHRYN  PQLVITGGPG  AEAYEQLAKN  ATTIDLTVDN  GNIRTSGEKQ
151 METLIARIFGK  EARAELKAQ  IDALFAQTRE  AAKGKGRGLV  LSVTGNKVSA
201 FGTQSRLASW  IHGDIGLPPV  DESLRNEGHG  QPVSFYEIKE  KNPDWIFIID
251 RTAAIGQEGP  AAVEVLNLDN  ALVRGTNAWK  RKQIIVMPAAN  YIVAGGSRQLI
301 QAAEQLKEAF  EKAEPVAAAG  E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

```

a750.pep  10      20      30      40      50      60
VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60

a750.pep  70      80      90      100     110     120
AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
          70      80      90      100     110     120
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
          70      80      90      100     110     120

```

	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
m750	130	140	150	160	170	180
a750.pep	190	200	210	220	230	240
m750	190	200	210	220	230	240
a750.pep	250	260	270	280	290	300
m750	250	260	270	280	290	300
a750.pep	310	320				
m750	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

1	ATGGCTTGGA	GTATGTTTGC	CACAACCCAA	GCCGATAGAG	CGGTAAGGTC
51	TGCAACTGCA	CCTAAAGAAA	TGTGGTTCCA	TAAGAAGATA	ATAGATGAAA
101	AAACAGGTAA	AGTATCCTTT	GATACCAGAC	AAATTTGGTC	ATTGAATGAT
151	TTAAGCAAGG	AAGAACTGGC	AAGCATTCAA	GACACAAATG	GCAAAGTTAT
201	TACTGTGTCT	AATCCTGGTA	TTTTCAATAA	TCGAGAAGAT	TCATTAAGCA
251	ACGCAGCAAA	ACAAAATCGT	AATAGTACAA	ACGGTAGTGG	TGTTATTGCA
301	GTCTGAATC	CTCCAACAGG	GAAATATAAA	TCTGATTCTA	ATAACAAAAT
351	AAAAGATTTT	TTATGGCTCG	GTTCAAGTCT	TGTTTCTGAA	CTGATGTATG
401	TCGGTTACGA	CCAATTAAAT	AATAAAGTGT	TCCAAGGCTA	TTTACCCAAA
451	ACCAATTGAG	AAAACTGAA	TCAAGATATT	TATCGAGAGG	TTCAAAAAAT
501	GGGTAACGGC	TGGTCGGTTG	ATACCAGTAA	TCACAGTCGT	GGGGGAATTA
551	CAGCAAGCGT	TTCTTAAAA	GATTGGGTAA	ACAATCAAAA	ACAAAATGGC
601	ATTGCCCCAA	TCAGAAAAGC	ACGTTTCTAT	GGTACAGCCA	CAAATGTGCA
651	GAATGATTAC	GCCGATGTTT	TACAGAAAAA	CGGCTATACC	TATACGGGTG
701	CAGACGGCAA	AACCTTATAAC	AGCGGATCCT	ACTCAATCGT	GCATGATAAA
751	GATTTTGTGG	GGAACAAATG	GATACCTTTC	TTGCTAGGAA	CCAATGACAC
801	CACACAAGGT	ACATGTAAGG	GGTTGTGCTA	TTGCGATAGC	AGTTATTTTG
851	CGGAGGTGCC	AAAAGCAGGT	ACAAAAGAAT	TTGATGACTA	TGTAAAAATA
901	TGGGGTGAA	TTGAATATGA	CGCTCAAGGT	AAGCCAATTA	ACAAATCTAA
951	ACCCATACTG	GTAGAACCAA	ACAAAACAAA	AGATAATGAA	AAATATGAAA
1001	AAGAAGCTTT	CTAA			

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

1	MAWSMFATQ	ADRAVRSATA	PKEMWFHKKI	IDEKTGKVSF	DTRQIWSLND
51	LSKEELASIQ	DINGKVITVS	NPGIFNNRED	SLSNAKQNR	NSTNGSGVIA
101	VMNPPTGKYK	SDSNKIKDF	LWLGSLLVSE	LMYVGVDQLN	NKVFGQYLPK
151	TNSEKLNQDI	YREVQKMGNG	WSVDTSNHSR	GGITASVSLK	DWVNNQKQNG
201	IAPIRKARFY	GTATNVQNDY	ADVLQKNGYT	YTGADGKTYN	SGSYSIVHDK
251	DFVGNKWIPF	LLGTNDTTQG	TCKGLCYSHS	SYFAEVPKAG	TKEFDDYVKI
301	WGEVEYDAQG	KPINKSKPIL	VEPNKTKDNE	KYEKEAF*	

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
  1 ATGAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATCTCT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CGCGCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAATCC GTTTATCCAT CCGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA GTTTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
  1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
 51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTIFYIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
  1 ATGAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATCTCT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
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1228

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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTC TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTC GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFWCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVKAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGO FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTCG GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPLPNII SPKLYPNEQW NESEALGAIW WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCGCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTAA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAA ATTGACTGAA CGGGATTTGC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTGCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGCGCATG CACACCTCAA AAATTTTTCG TACTCTATC ATGACGAATA
951 CGATGTTTCG CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYP FAYDNPNSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLEGINARQ
151 VFQQYMAEIF HHGRFVSVSQ IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAA NEFLC MQTIKQAGIA VAQTSLS EDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKKTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQRVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*

```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTTCGTG AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1 MTANFAQTLV EIQDSLVRV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVPYGA E LVSDGNFTAV LSDIGD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTTCGTG AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1 MTANFAQTLV EIQDSLVRV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVPYGA E LVSDGNFTAV LSDIGD*

```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLVRVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAAC TGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGCGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADE	LQYVWEHTAVTDHQGKLVEI	PVCYGGGEYGPDLAEVAAFHQ			
a758	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADE	LQYVWEHTAVTDHQGKLVEI	PVCYGGGEYGPDLAEVAAFHQ			
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMM	GFQPGFPYLGGLPEALHTPR	RAVPRTSVPA	GSVGIGGSQT		
a758	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMM	GFQPGFPYLGGLPEALHTPR	RAVPRTSVPA	GSVGIGGSQT		
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP	LFRADLNPPPTLLAAGDQVRF	VAERIEPX			
a758	130	140	150	160		
	GVYPFASPGGWQIIGRTELP	LFRADLNPPPTLLAAGDQVRF	VAERIEPX			

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCTCGG
 51  TCTTTTGGCC GTTTCCTCTG CTTACTCATC CATTGTCCGC AACGATGTGC
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCAACGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAGAA TATTAGGCAG
201  GGTTCACAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCAGCCAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAAGC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
651 AAACCACGGC TTA CTGCTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTGACAAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
801 CGATAATTTT TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
901 GAACTCATAT GCGCGACAAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCTGCT CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTCACCGTC GTCGGTAAAA
1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
1301 TCGGGGAAGG CACTGTGCTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCATATC
1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCT
1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTCAGAA
1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CCGCGCGAAT TTTTCCCCTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
1901 AAGCAGCCAT AGAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTAGGCAG GCCCGTACCC
2101 CATGCCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGTACCGC TCCTACCATA GCGGCAGCAC CCACCTGCAC CCCAACGCCG
2351 TTTTAAAAGC CGAAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
2551 GACGGCGCAC AAATTACCCG GAACCCGAT TTCGCCAATA ATACACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCCGGC
2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAACCTGGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAAAACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACCTGTG AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTCAACC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAAACAACG GATACAGCCT
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
3151 CGTGCCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGGTAGAAA TGGCCGAATC CGAATTGAC
3301 AAAGCACGGC AAGGCGGCGA TCGCAAGCC GTCGAAACAG CCCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAATC GATCAGCCGG
3451 TCGGCCAACA CCGCGTTTTC CGAACAGGCC GCCTACAATA CCGGCGGCGA
3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

m759.pep

```

1  MRFTHTTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51  GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLL G NGQPKANAYL DTD RFPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGT P LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER I TLP IANPSL APQND SRHMP SEDAGKTLIL
351 SSRFDNK TLM LADNINOGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKL GAGTL IANGQGINQG DISIGETVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
501 RHADGGAQIV NHNPDAQATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNGEV LIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQKTP ECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLGKAHLYGS IRAGKDTAVR MEADSNW TLS QSSHTGALT L
851 DGAQITLNP D FANNT HNNRF NTLTVNGTLD GFGTFRFLT G IVRKQNA PPL
901 KLEGDSRGAF QIHVKNTGQE PQTTE SLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVOYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAELISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQOTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE D GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

g760.seq (partial)

```

1  AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51  CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCGCG GTCCGGCGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

g760.pep (partial)

```

1  NNRNTRYAAL GKRVMEGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51  DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTTC GCACACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGCGACG CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCC GACCAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAAATGC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTTCCGCG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCCG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCGCAT TGGGCAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAAATCCA TGCAGTTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCCG
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGACGGGAT ACATGCAGGC
1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATT CCGGTTTCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVERI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQOVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFAFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGLYQQR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNTYFA GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLSKSVLD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYFRMKDKNAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSESTFNIPGSESLTANL					
g760	AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSTNTFNIPGSESLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq					
1	ATGAAATAT	CATTTCAATT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTCCT	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTACCCGGC	GAAGTCGGGC	GCGCCAAATC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTA
701	CCGTCAAACT	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTTGAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGG
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTC	AAATTCTGTC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTACGCCCCA	ACATCGCGCG
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTGAGCAT	CGATACGTTG
1501	TCTTCGCGCG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA


```

1701  ATTGTCCGCC  ATCGGGCAAA  TCATCCCCAA  AAAACTCTAT  CTGCGCGGTT
1751  CGTTGGGCGT  GATGCAGGCG  AAAGTCGTTG  AAGACAAAGA  AAATCCCGAC
1801  CGAGTGGGCA  TCCATTTGAA  TAATACCAGC  AACGTTACCG  GCAACCTGTT
1851  TTTCCGTTAT  ACCCCGACCG  AAAACCTCTA  CGGCGAAATC  GGCCTAACCG
1901  GTACAGGCAA  ACGCTACGGT  TACAACCTAA  GAAATAAAGA  AGTGACTACG
1951  CTTCCAGGCT  TTGCCCCAGT  TGATGCCATG  CTTGCGTGGA  ACCATAAAAA
2001  TGTTAACGTT  ACCTTTGCCG  CAGCCAATCT  GCTCAATCAA  AAATATTGGC
2051  GTTCGGACTC  TATGCCGGGT  AATCCGCGCG  GCTATACTGC  CCGGGTAAAT
2101  TACCGTTTCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1  MKISFHLALL  PTLIIASFPV  AAADTDNNGE  HYTATLPTVS  VVGQSDTSVL
51  KGYINYDEAA  VTRNGQLIKE  TPQITIDTLNI  QKNKNYGTND  LSSILEGNAG
101  IDAAYDMRGE  SIFLRGFQAD  ASDIYRDGVR  ESGQVRRSTA  NIERVEILKG
151  PSSVLYGRTN  GGGVINMVS  YANFKQSRNI  GAVYGSWANR  SLNMDINEVL
201  NKNVAIRLTG  EVGRANSFRS  GIDSKNVMVS  PSITVKLDNG  LKWTGQYTYD
251  NVERTPDRSP  TKSVDYDRFGL  PYRMGFAHRN  DFKVDKLQVW  RSDLEYAFND
301  KWRAQWQLAH  RTAAQDFDHF  YAGSENGNLI  KRNYAQOQTD  NKTLSNLT
351  NGDYITGRFE  NHLTVGMDYS  REHRNPTLGF  SSASFASINP  YDRASWPASG
401  RLQPILTQNR  HKADSYGIFV  QNIFSATPDL  KFVLGGRYDK  YTFNSNKLT
451  GSSRQYSGHS  FSPNIGAVWN  INPVHTLYAS  YNKGFPYGG  RGGYLSIDTL
501  SSAVFNADPE  YTRQYETGVK  SSWLDDRLST  TLSAYQIERF  NIRYRPDPKN
551  NPYIYAVSGK  HRSRGVELSA  IGQIIPKKLY  LRSLGVMQA  KVVEDKENPD
601  RVGIHLNNTS  NVTGNLFFRY  TPTENLYGEI  GVTGTGKRYG  YNSRNKEVTT
651  LPGFARVDAM  LGWNHKNVNV  TFAANLLNQ  KYWRSDSMPG  NPRGYTARVN
701  YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1  ATGAAAATAT  CATTTCATTT  AGCTTTATTA  CCCACGCTGA  TTATTGCTTC
51  CTTCCCTGTT  GCTGCCGCCG  ATACGCAGGA  CAATGGTGAA  CATTACACCG
101  CCACTCTGCC  CACCGTTTCC  GTGGTCGGAC  AGTCCGACAC  CAGCGTACTC
151  AAAGGCTACA  TCAACTACGA  CGAAGCCGCC  GTTACCCGCA  ACGGACAGCT
201  CATCAAAGAA  ACGCCGCAAA  CCATCGATAC  GCTCAATATC  CAGAAAAACA
251  AAAATTACGG  CACGAACGAT  TTGAGTTCCA  TCCTCGAAGG  CAATGCCGGC
301  ATCGACGCCG  CCTACGATAT  GCGCGGCGAA  AGCATTTTCC  TGC GCGGCTT
351  TCAAGCCGAC  GCATCTGATA  TTTACCGCGA  CGGCGTACGC  GAAAGCGGGC
401  AGGTGCGCCG  TAGCACCGCC  AACATCGAGC  GCGTGGAAAT  CCTGAAAGGT
451  CCGTCCTCCG  TGCTTTATGG  GCGTACCAAC  GCGCGCGGTG  TCATCAACAT
501  GGTCAGCAA  TACGCCAACT  TCAAACAAAG  CCGTAATATC  GGTACGGTTT
551  ATGGTTTCGTG  GGCAAACCGC  AGCCTGAATA  TGGACATCAA  CGAAGTGCTG
601  AACAAAACG  TCGCCATCCG  TCTACCGGC  GAAGTCGGGC  GCGCCAATTC
651  GTTCCGCAGC  GGCATAGACA  GCAAAATGT  CATGGTTTCG  CCCAGCATT
701  CCGTCAAAC  CGACAACGGC  TTGAAGTGGA  CGGGGCAATA  CACCTACGAC
751  AATGTGGAGC  GCACGCCGCA  CCGCAGTCCG  ACCAAGTCCG  TGTACGACCG
801  CTTCCGACTG  CCTTACCGCA  TGGGGTTCGC  CCACCGGAAC  GATTTTGTCA
851  AAGACAAGCT  GCAAGTTTGG  CGTCCGACC  TTGAATACGC  CTTCAACGAC
901  AAATGGCGTG  CCCAATGGCA  GCTCGCCAC  CGCACGGCGG  CGCAGGATTT
951  TGATCATTT  TATGCAGGCA  GCGAAAATGG  CAACTTAATC  AAACGTAAC
1001  ACGCCTGGCA  GCAGACCGAC  AACAAAACCC  TGTCTGTC  CTTAACGCTC
1051  AACGGCGACT  ACACCATCGG  CCGTTTGTAA  AACCACTGA  CCGTAGGCAT
1101  GGATTACAGC  CGCGAACACC  GCAACCCGAC  ATTGGGTTTC  AGCAGCGCCT
1151  TTTCCGCCTC  CATCAACCCC  TACGACCGCG  CAAGCTGGCC  GGCTTCGGGC
1201  AGATTGCAGC  CTATTCTGAC  CCAAAACCGC  CACAAAGCCG  ACTCCTACGG
1251  CATCTTTGTG  CAAAACATCT  TCTCCGCCAC  GCCCGATTG  AAATTCTGTC
1301  TCGGCGGCCG  TTACGACAAA  TACACCTTTA  ATTCCGAAAA  CAAACTCACC
1351  GGCAGCAGCC  GCCAATACAG  CGGACACTCG  TTCAGCCCCA  ACATCGGCGC
1401  AGTGTGGAAC  ATCAATCCCG  TCCACACACT  TTACGCCTCG  TATAACAAAG
1451  GCTTCGCGCC  TTATGGCGGA  CGCGGCGGCT  ATTTGAGCAT  CGATACGTTG
1501  TCTTCGCGCC  TGTTCAACGC  CGACCCCGAG  TACACCCGCC  AATACGAAAC
1551  CGGCGTGAAA  AGCAGTTGGC  TGGACGACCG  CCTCAGCACT  ACGTTGTCTG
1601  CCTACCAAAT  CGAACGCTTC  AATATCCGCT  ACCGCCCCGA  TCCAAAAAAC
1651  AACCCTTATA  TTTATGCGGT  TAGCGGCAAA  CACCGTTCGC  GCGGCGTGGA
1701  ATTGTCCGCC  ATCGGGCAAA  TCATCCCCAA  AAAACTCTAT  CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGGACCG AAAACCTCTA CGGCGAAATC GCGCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
 51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKVQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQT DNKTLSSNLTL
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAFAVDAM LGWNHKNVNV TFAAANLENQ KYWRSDSMPG NPRGYTARVN
701 YRF*

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m761 / a761 99.6% identity in 703 aa overlap

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              10      20      30      40      50      60
m761.pep      MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA
              |
a761           MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m761.pep      VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD
              |
a761           VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD
              70      80      90      100     110     120

              130     140     150     160     170     180
m761.pep      ASDIYRDGVRESGQVRRSTANIERVEILKGPSVLYGRTNNGGGVINMVS K YANFKQSRNI
              |
a761           ASDIYRDGVRESGQVRRSTANIERVEILKGPSVLYGRTNNGGGVINMVS K YANFKQSRNI
              130     140     150     160     170     180

              190     200     210     220     230     240
m761.pep      GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG
              |
a761           GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG
              190     200     210     220     230     240

              250     260     270     280     290     300
m761.pep      LKWTGQYTYDNVERTPDRSP TKSVDYDRFGLPYRMGFAHRNDFVKDKLQVW RSDLEYAFND
              |
a761           LKWTGQYTYDNVERTPDRSP TKSVDYDRFGLPYRMGFAHRNDFVKDKLQVW RSDLEYAFND
              250     260     270     280     290     300

              310     320     330     340     350     360
m761.pep      KWRAQWQLAHR TAAQDFDHFYAGSENGNLIK RNYAQQT DNKTLSSNLTLNGDYTIGRFE
              |
a761           KWRAQWQLAHR TAAQDFDHFYAGSENGNLIK RNYAQQT DNKTLSSNLTLNGDYTIGRFE
              310     320     330     340     350     360

              370     380     390     400     410     420

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1239

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m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761       NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761       QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
a761       YNKGFPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761       NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761       RVGIHLNNTSNVTGNLFFRYTPPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761       LGWNHKNVNVTFAAANLNFNQKYWRSDSMPGNPRGYTARVNYRFX
           670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLFIFNEV TKSIIYMAIY PILYFFTICK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGCG
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTAC CTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
 251 CAGTGC GCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCCT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCGGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACGG TATTTGCGGA
 1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQROP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACG GTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCG CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CCGTGCGGCG CGTTACCAAA TCATGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTCGCGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQROP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

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m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSA	DFQASHYQ	ORDAVRAR	QQQAKAA	FLPHVSA	NASYQRQPP
a763	LPEAWRAAQHSA	DFQASHYQ	ORDAVRAR	QQQAKAA	FLPHVSA	NASYQRQPP
	70	80	90	100	110	120
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLF	DAAKFAQY	RQSRFDTQ	AAEQRFDA	AREELLK	VAESYFNV
a763	GWSVQVGQTLF	DAAKFAQY	RQSRFDTQ	AAEQRFDA	AREELLK	VAESYFNV
	130	140	150	160	170	180
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQ	VRQAQAL	FNKGAATA	LDIHEAKA	GYDNALA	QEIAVLA
a763	HAAEKEAYAQQ	VRQAQAL	FNKGAATA	LDIHEAKA	GYDNALA	QEIAVLA
	190	200	210	220	230	240
m763.pep	250	260	270	280	290	300
	TDLDSKQIEA	IDTANLLA	RYLPKLE	RYSLDEW	QRIALS	SNNHEYR
a763	TGLDSKQIEA	IDTANLLA	RYLPKLE	RYSLDEW	QRIALS	SNNHEYR
	250	260	270	280	290	300
m763.pep	310	320	330	340	350	360
	QNSRYPTVSA	HVGYQNN	LYTSSAQ	NNDYHYR	GKGMSV	GVQLNL
a763	QNSRYPTVSA	HVGYQNN	LYTSSAQ	NNDYHYR	GKGMSV	GVQLNL
	310	320	330	340	350	360
m763.pep	370	380	390	400	410	420
	OYGAAEAQLT	ATERHIK	LAVRQAY	TESGAAR	YQIMAQ	ERVLESS
a763	OYGAAEAQLT	ATERHIK	LAVRQAY	TESGAAR	YQIMAQ	ERVLESS
	370	380	390	400	410	420
m763.pep	430	440	450	460		
	NRLEVIRARQ	EVAQAEQ	KLAQARY	KFMLAYL	RLVKES	GLGLET
a763	NRLEVIRARQ	EVAQAEQ	KLAQARY	KFMLAYL	RLVKES	GLGLET
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

m764.seq

```

1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGTTTTTGT CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGCGG
251 CTTCGGGCAA AACGGTGTCG GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAATGG ACCTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

m764.pep

```

1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEOAFL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSA LRGHQ AELQSAKAE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAADD DKMDVEVLVL NKDIGFEVQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

a764.seq (partial)

```

1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAAGT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGTTTTTGT CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGCGG
251 CTTCGGGCAA AACGGTGTCG GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA

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701 CAGCAGACTA CCGCCGTTTG CGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

a764.pep (partial)

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVVRDQHVKGGE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVVRDQHVKGGE					
	70	80	90	100	110	120
m764.pep	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
	130	140	150	160	170	180
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQKLVSVAIEQQKTADYRRL					
a764	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQKLVSVAIEQQKTADYRRL					
	190	200	210	220	230	240
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVAPDD					
	310	320	330	340	350	360
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					

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|||||
a764 DKMDVEVLVLNKGDFVEQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
      370      380      390      400      410      420

      430      440      450      460      470
m764.ppep AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFREXR
          |||||
a764 AVVSLDKHTLNIDGK
          430
```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGCG CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```
m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGKKNVGGQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGYGLTL PYSRSLIEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLIPTVM PVYEQSVRNK
301 GRVNRKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACCGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```
a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
```

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```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDGEIAAI MGHEMTHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLPTVM PVYEHVSRNK
301 GRVKNRNR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPSVLDSDGIFLKFNF	FLRSKPKYEISFLPSFKRIL	CLSAVISVLGACAVVADVYG			
a765	MLRCRPSVLDSDGIFLKFNF	FLRSKPKYEISFLPSFKRIL	CLSAVISVLGACTVADVYG			
	10	20	30	40	50	60
m765.pep	HDSATMNAAA	AKDYMKTVELNKSAGNVD	TTSRTARRVQAVFRRMLPY	ADAANNTSHKFDW		
a765	QDSATMNAAA	AEDYMKTVELNKSAGNVD	TTSRTARRVQAVFRRMLPY	ADAANNTGHKFDW		
	70	80	90	100	110	120
m765.pep	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDDEIAAIMGHEMTHAL	HEHGKKNVQGO		
a765	KMTVFKNDEL	NAWAMPGGKMAFYTGIVDKL	KLTDGEIAAIMGHEMTHAL	HEHGKKNVQGO		
	130	140	150	160	170	180
m765.pep	ILTNMAAQIG	TQIILDKKPD	TNPVLVGLGMDILGTYGL	TLPYSRSL EEEA	DEGGMLMAQ	
a765	ILTNMAAQIG	TQIILDKKPD	TNPVLVGLGMDILGMYGI	TLPYSRSL EEEA	DEGGMLMAQ	
	190	200	210	220	230	240
m765.pep	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIE	NLKRLPTVMPVYEQSV	RNK	
a765	AGYHPAAAVR	VWEKMNQENDQNGFIYAIT	STHPTNNARIE	NLKRLPTVMPVYEHV	SRNK	
	250	260	270	280	290	300
m765.pep	GRVKNRNR					
a765	GRVKNRNR					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTTG TTGGATAAAC
101 CCATTCTCA AGAACAGCCG GGAATAATG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAAAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAAGTATGTC GCGCCTATGA TTCCCCGAA
451 GCTGCCCGCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GGTGCGCAAA
601 GTCAGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQP GKIEVLEFFG
51  YFCVHCHHFD PLLKLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKAVYEQKIR LENRAVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAVALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCTCA AGAACAGTCG GGTAATAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTGTCTG
 301 GGTGTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
 451 GCTGCCGCCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTGCGCAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
 101 GLKYQANPAV FKAVYEQKIR LENRSVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	SAVLSAQAYAL	TEGEDYLVLD	KPIPQEQSGK	IEVLEFFGYF	CVHCHHFD
m767	MKLKHLLPLL	SAVLSAQAYAL	TEGEDYLVLD	KPIPQEQSGK	IEVLEFFGYF	CVHCHHFD
	10	20	30	40	50	60
g767.pep	70	80	90	100	110	120
g767.pep	PLLLKLGKAL	PSDYLRTHEV	VWRPEMLGL	ARMMAAVKLS	GLKYQANSV	FKAVYEQKIR
m767	PLLLKLGKAL	PSDAYLRTEH	VVWQPEMLG	LARMAAVNLS	GLKYQANPAV	FKAVYEQKIR
	70	80	90	100	110	120
g767.pep	130	140	150	160	170	180
g767.pep	LENRAVAGKW	ALSQKGFDDG	KLMRAYDSPE	AAAAVALKMQ	KLTEQYRIDST	PTVIVGGKYR
m767	LENRSVAGKW	ALSQKGFDDG	KLMRAYDSPE	AAAAAALKMQ	KLTEQYRIDST	PTVIVGGKYR
	130	140	150	160	170	180
g767.pep	190	200	210			
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGAATAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTACGA CTCTCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
51  YFCVHCHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKA VYEQKIR LENRSVAEKW ALSQKGFQDG KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLLPLL SAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL SAVLSAQAYALTEGEDYLVLDKPIPOEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a767.pep	PLLLKLKALPSDAYLRTEHV VVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR					
m767	PLLLKLKALPSDAYLRTEHV VVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a767.pep	LENRSVAEKWALSQKGFQDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR					
m767	LENRSVAGKWALSQKGFQDGKLMRAYDSPEAAAAALKMOKLTEQYRIDSTPTVIVGGKRYR					
	130	140	150	160	170	180
	190	200	210			
a767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKOLITAA LIASAAFATQ AAPQKPVSA QTAQSAVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGKMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP		
m768	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP		
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIEAAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
m768	VDQIVRRIHEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATAACAGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP		
m768	MNIKHLITAALIASAAFAAQAA	PQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP		
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIEAAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
m768	VDQIVRRIHEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```
1   TTGATAATGG TTATTTTTTA TTTTATTTTT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAgaAAC ACCgtgCGAA CCGGATTGTA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCTG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCCATT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCGA AACGAGGCGG CCGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGCGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAACA GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACG CGGGCGGCGA
801 CGTGTCGGCG AGGGTTTATC CGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCGACA ATACCCATT GCAAATTTCC AATTCGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTTAC CCGCAGCGCA
1151 ACCCCGCGCA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAG AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```
1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQGVRE KGVVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPQL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQEWGGSGL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```
1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGAAGAA GGAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAACAAT
301 ATTGCCGTTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAAATTGAT TGCCGCCCAA
451 CCCGACGCGC CCGCGTCCG TATGCCGTTG CCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGC ATGCGTGGA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCACCAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAAACCCG AAATGGCAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
```

1251

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1251  GGC GAAACGG CATTATGAAA AACCCGGCTT TTCAGCGGT TTTAAAGGGG
1301  AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACC GG
1351  GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACC GCGA
1401  AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451  TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
1    LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51   HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSVVSN
101  IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151  PDAPAVRMRL AAALFENRON EAAADQFDR LKAENLPPQLM EQVELYRKAL
201  RERDAWKVNG GFSVTREHNI NQAPKRQYQ KWTFFPKQVDG TAVNYRLGAE
251  KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301  AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351  SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401  GQEWGSGSLG SLLRLGAAKR HYEKPGFFSG FKGERRRDK E LNTSLSLWHR
451  ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769    95.1% identity in 492 aa overlap

          10      20      30      40      50      59
g769.pep    LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI
          |||||  |||||  |||||  |||||  |||||  |||||
m769        LIMVIFY--FCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPI
          10      20      30      40      50

          60      70      80      90     100     110     119
g769.pep    DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
          |||||  |||||  |||||  |||||  |||||  |||||
m769        DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
          60      70      80      90     100     110

          120     130     140     150     160     170     179
g769.pep    KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD
          |||||  |||||  |||||  |||||  |||||  |||||
m769        KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD
          120     130     140     150     160     170

          180     190     200     210     220     230     239
g769.pep    RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYGNWTFPKQV
          |||||  |||||  |||||  |||||  |||||  |||||
m769        RLKAEENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYGNWTFPKQV
          180     190     200     210     220     230

          240     250     260     270     280     290     299
g769.pep    DGTAVNYRFGAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
          |||||  |||||  |||||  |||||  |||||  |||||
m769        DGTAVNYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
          240     250     260     270     280     290

          300     310     320     330     340     350     359
g769.pep    GLAVFHERRTYGNDAYSANGARLYFNRWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI
          |||||  |||||  |||||  |||||  |||||  |||||
m769        GLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI
          300     310     320     330     340     350

          360     370     380     390     400     410     419
g769.pep    SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLFRLGVA
          |||||  |||||  |||||  |||||  |||||  |||||
m769        SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGAA
          360     370     380     390     400     410

          420     430     440     450     460     470     479
g769.pep    KRHYEKP GFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
          |||||  |||||  |||||  |||||  |||||  |||||

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m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep   KNRAVFVEFNKTFX
          |||||
m769      KNRAVFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCCGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAATTGAT TGTGCCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCACTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGC ATGCGTGGAA GGTAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAAATATC AACCAGCCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAAG TGCCGGGCTG
901 GCAGTGTTCG ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 GCTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCTGTCT TCGCTGTTGC GCCTCGGCCG
1251 GGCGAAACGG CATTATGAAA AACCAGGCTT TTTCAGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGTGAT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTG TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKROQYG KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWGY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAARK HYEKPFFSG FKGERRRDK E LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep   LIMVIFYFCGKTFMPARNRWMLLLPLLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep   EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

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|||||
m769      EKVPGQVREKGVQLIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
              70          80          90          100          110          120

              130          140          150          160          170          180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAVAVRMRLAAALFENRQNEAAADQFDRL
              130          140          150          160          170          180

              190          200          210          220          230          240
a769.pep   KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQYQKWTFFPKQVDG
|||||
m769      KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQYQKWTFFPKQVDG
              190          200          210          220          230          240

              250          260          270          280          290          300
a769.pep   TAVNYRLGAEEKWLSLKNWYTTAGGDVSGRVYPGNKKFNMDTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKWLSLKNWYTTAGGDVSGRVYPGNKKFNMDTAGVSGGIGFADRRKDAGL
              250          260          270          280          290          300

              310          320          330          340          350          360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLNTRRARSNDNTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLNTRRARSNDNTHLQISN
              310          320          330          340          350          360

              370          380          390          400          410          420
a769.pep   SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAKR
|||||
m769      SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAKR
              370          380          390          400          410          420

              430          440          450          460          470          480
a769.pep   HYEKPGFFSGFKGERRRDKELNLSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
|||||
m769      HYEKPGFFSGFKGERRRDKELNLSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN
              430          440          450          460          470          480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AAGCGCGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTTC GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCGGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1   MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTFGA FKSQIVRY YDPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

g770.pep      10      20      30      40      50      60
MNRLLLLSAAVLPTACGSGETDKIGRASTVFNMLGKNDR I EVEGFDDPDVQGVACYISYA
|||||
m770          10      20      30      40      50      60
MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
|||||

g770.pep      70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKRGTFGFAFKSRQIVRY Y
|||||
m770          70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKHGASFAFKSRQIVRY Y
|||||

g770.pep      130     140     150     160     170     180
DPKRKAFA YLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
|||||
m770          130     140     150     160     170     180
DPKRKTFA YLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
|||||

g770.pep      KNPDKRX
               :| |||
m770          ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC

```

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

a770.pep	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
m770	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASF AFKSRQIVRY
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASF AFKSRQIVRY
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
a770.pep	ENPDKRX
m770	ENLDKRX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAAAC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTGAAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTGCTCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTGCCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGCCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCGG

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1751 GGAAATCTC GGGCAGCACA CCCTTCTACC GATTCACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAUVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTHRKISFD ADIRRRLLFR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQOFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNGLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAALQ KLNLA PYLDE FRQONGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQGSL SLNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGTGTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAGCATT
151 GCACACACAC ACCGGAAAAT CTCGTTTGAT GCGGCATTTC AGCGCAGGCT
201 CCTGCCCCCG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAAAC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 TCGAAAAACA GCACGTCCTG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGG TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTTCGCTGGA CGGACACGGC ATTACCATT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTC AGGGCTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGGCA CGCGGTATC GACCTGACCG CGGGCGGCGA AACC CGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACG
1801 CTTCAACAGCG AATTTTCTAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTCTCTCCAG AGCCTCTATG TTACCGAGCA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGG ACGGTGGACA AACC GTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTTC CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 ANTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQLDDME TYLHADKQHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS SLNISGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
              10      20      30      40      50      60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
          10      20      30      40      50      60

              70      80      90      100     110     120
g771.pep ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVSGAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLTITEPGGDOTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
          70      80      90      100     110     120

              130     140     150     160     170     180
g771.pep LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNLFQQQLILKEISLNLQSPDSS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQLILKEINLNLQSPDSS
          130     140     150     160     170     180

              190     200     210     220     230     240
g771.pep GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
          190     200     210     220     230     240

              250     260     270     280     290     300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
          250     260     270     280     290     300

              310     320     330     340     350     360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDNGLDAPRLHISTLQD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
          310     320     330     340     350     360

              370     380     390     400     410     420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFYKTREGAPHLEAAAAALQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVSNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
          370     380     390     400     410     420

              430     440     450     460     470     480
g771.pep KLNLAHYLDEFQONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKQHI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKQHI
```

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHDITELFSDSLVYTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHDITELFSDSLVYTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCATCTT	CACACCTGAA	AACATCCGAA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAAT	CTCGTTGAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCCGG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGAAAAAACC	TGTGGTCGGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGCGGAA	CTTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGGAAC	AGCTTATCCT
501	GAAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTCTGTC	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGGAAG
601	AGCAGGGGGC	TGTTCTTTTC	AGACGGCATC	GGCAGCCCCA	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATTACCATTT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGCGCG	AGCGGATGCC
751	GCCGCGCTCG	GCCTGCGTGC	AGACACTTCC	TTCGCGCAAC	TCCACCTGAC
801	CGCCCAAAAT	CCTACGCTGG	CACTCAGGAA	CAACAGCATT	AAAATTGAAA
851	CCGTCACACG	CGCATTACCC	GCCGCGCGCG	AATATGCCCA	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGCGATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCTCCCTCAA	TTCCGCGCTC	GTATGGACGG	AAAACAAAGG	GCTGGACGCG
1051	CCGCGCCTGT	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATTCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCT	GACACCCTCG	CCAAGCTGTC	CGGCGACATC
1351	GAGGCGCACC	TGAAAATCGG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGGCCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	CGCGGTCATC	GACCTGACCG	CGGGCGGCGA	AACCCGAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGCAGCCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCGG
1751	GCAAACTGTC	CGACAATGCC	GCACCCAGCA	CACCCCTCCA	CCGATTACAG
1801	CTCAACAGCG	AAATTTCAGA	CGGCATCAGC	CGCCACATCG	ATACCGAACT
1851	CTTCTCCGAC	AGCCTCTATG	TTACAGCAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GTCTGAAGAT	GTCCTTATCC	GCAACGCCGT	CCATCCGAAA
1951	AACAACCCGA	TTCCCTGAA	AATACCGGT	ACGGTGGACA	AACCGTCCAT
2001	TACCGTCGAT	TACGGCAGGC	TGACCGGCGG	CATCAATTCC	CGCAAGAGAG
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAAGAAC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

a771.pep

```

1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EHLKIGKVQ LPLQLDDME TYLHADKGIH ALSRFKSGLY GGHTGGGSI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKEIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILE TLLEQWQWLK
701 PKEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLLAAGLHASVYRIFTPE	NIRSRLQOSIAHTRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLLAAGLHASVYRTFTPE	NIRSRLQOSIAHTRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE	
m771	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE	
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLNQSPDSS	
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLNQSPDSS	
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHF	EASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHF	EASTSLDGHGITISTTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTALRNNSIKIETVNGAFTAGGEYAQWDG	
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG	
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQWNNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSV PNLQWNNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ
a771.pep	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EHLKIGKVQLPGLQLDDMETYLHADKGIH
m771	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EHLKIGKVQLPGLQLDDMETYLHADKGIH

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNIIKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNIIKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```
g772.seq
1 GTGTTTCGGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51 CGTCGGGCAAG TTCTTTTCAGG TTGTTTCGTA TGGTTTTTCGG GCGTTTGGCGG
101 AAGGCGCAATT TCACCAAGTTT TGGCGAAATGA TCGAAAATCGT GCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 CGCGGGGATC GAACGATTTCG GGGCGGACGT CAATCAGCAG CTCCATATCG
251 AAAAAAATATT GCAGCATCAC ACCCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGGGGACATC GTCGCGCAC TCCGCCAGTT TGAACAAAG CGGCGTGGAG
401 ATGTTTATACG GCAGGTTGCC GACGATTTTC TTTTTCGGTG AGATGCGGTT
451 GAAATCAAAC TGCAATCACGT GCGCTTCGTG AATCAGCAT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATAACGATGTC GCGGTCGAT TTTCGACAACG
551 TGCAGGCGGT TACGCTTTTTT CGGCCAAAGT TCGGTAATTG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGGCG ACCGGGTTGA
651 CAATATCCGC GATAATCCGC GTGTCTGCA AAAAATCTG CCGGAAATCG
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTCTTCGGT TGAAACCCCG
751 CCTTTTAGGG CGCGAGGATA AGACTCTGTT TGGGCGGGGC GTAAACCCCTT
801 CCAATACAGG ACGACACATA GCGGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pap

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	EFRGRHVNQQ	LHIEKILQHH	TOATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGVDVIRQA	DFDLFA*DAV
151	EIKLQHVAVF	NHOFIRKQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGCRQT
201	RADFNDHIIR	LRAHGVDNIA	DNPRVLQKIL	PETLAGVFFF	HRVSSSVETP
251	PFRAGSDSV	WAGRNPFQIR	THRAVLVYS	SCVLEHKCVY	SIRLMSLA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTCCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTTGCCTA TGGTTTTCGC GCGTTCGGTG
101 AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CGCCTTTCGC
151 GATCGGGTGT TTCACCGGAA TCATACGGAG GACGGCGGAA TCCACTTTCG
201 CGCAGAGGTC GAACGATTCT GCGGGTACGT CAATCAGCAT TTCCATATCG
251 AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGGCAACC ATACGCTCGA CCACCTCTTT TTGCAGATAA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCGCGCAGCT TGAACAAAAG CCGTGTGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTGCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAAT TTATCCGCA
501 ACCGCGACGT TTTAGACGGG CATACGATGT CGCGTTCGAT TTCGACAACG
551 TGCAGCCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC GTCGGGCGCG CCGCGCTTGA
651 CAATATCGCT GATAATCCGC GTGCTCTGCA AAAAATTTCT CGCCGAACG

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLOYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGRNRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNHAA					
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g772.pep	HCGIDFRRGIERFGRHVNOQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVERFGRYVNOHFHIEKILQHHAQAQVVAFRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
g772.pep	VRHLRQFEQKRRGDVIRQVADDFLFAFXDAVEIKLQHVAFVNHQFIRKRQRFQAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVDLFAFACDAVEIKLOYIAFVNHQFIRKRQRFQAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
g772.pep	FDNVQAVQLFRQRFGRNCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGRNRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTHRAVLVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTGCG CGCTTGGTGG
101 AAGCGAGATT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCACGT CAATCAGCAT TTCCATATCG
251 AAGAATATT GCAGCATCAC GCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATCTG CCCGAAACGC
701 TTGCGGGGCT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
  1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51 DTVFHRNHAD DGRHFRRGV ERFGRHVNQH FHIEEILQHH AQAAVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLOYIAFV NHQFIRKQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD					
m772						
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRHFRRGVVERFGRHVNQHFIHIEEILQHHAQAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI					
m772						
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLOYIAFVNHQFIRKQRQFQTAYDVAVD					
m772						
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF					
m772						
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX					
m772						
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
  1 ATGGGATTGG GTGCAACGAC TTTTGTGCGT TCGGGTGCTA TAGGCGGAGG
 51 TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCTGTGCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAACATTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGCGAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAATTAC GGAGATCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
  1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
 51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101  TGVKTSLTPK TADVQRNLS QSEVGIKWGK GIEGQMPWE DYVGKGLSAN
151  ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGYIDK
201  TANFKSYELS EVPLRADMIK OREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251  NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
  1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
 51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101  CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAATATGTTA AACGGGAAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251  CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401  TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
  1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRTRYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201  QYRLQQKDIA RATWRSLIQT YPGSPAACKRA AAVVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
  1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCGCGCTC
 51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA
101  CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251  CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGCAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401  TTTCTGCCGC TGCCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
  1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201  QYRLQQKDIA RATWRSLIQT YPGSPAACKRA AAVVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

m774/g774 92.8% identity in 237 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

```

          10          20          30          40          50          60
a774.pep  MKTKLPLFIIWLSVSAACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT
          |||||||:|:|  :|:|  :|:|  :|:|  :|:|  :|:|  :|:|  :|:|  :|:|  :|:|
m774      MKIKLPLFIIWLSVSASCAS-VSPVPAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK
          10          20          30          40          50

```

1265

```

              70      80      90      100      110      120
a774.pep      LVRLSNEVELNGKVKALEHAKTHPSSRAYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQ
              :|||||
m774          IVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQ
              60      70      80      90      100      110

              130      140      150      160      170      180
a774.pep      NLYNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGNCESVIEIGGR
              :|||||
m774          NLYNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGNCESVIEIGGR
              120     130     140     150     160     170

              190      200      210      220      230      239
a774.pep      YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKRAAAVRKRXX
              :|||||
m774          YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKRAAAVRKRXX
              180     190     200     210     220     230
```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGTTGCTG GAGTCAAAAA ACGGTTTATG TCCGCGGCAC AGGCAAGAAG
851 CGGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGAGCCCG GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRS
51  YSNMFIGSSW KSPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTHNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPHP RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARSAVCF LRFWQATRGI PKTRSWRNPV NA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGGCCCTT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
```

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTTCGATTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDITI NNHHTHTHNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPHP ROEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

```

a790.pep      10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
|||||
m790          10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
|||||

a790.pep      70      80      90      100     110     120
GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
|||||
m790          70      80      90      100     110     120
GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV
|||||

a790.pep     130     140     150     160     170     180
LNDVQGDITI NNHHTHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA
|||||
m790         130     140     150     160     170     180
LNDVQGDITI NNHHTHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA
|||||

a790.pep     190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID
|||||
m790         190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPADEIALIELSDKRLVVAHLVID
|||||

a790.pep     250     260     270     280     290     300
IAGRMLIYQTRPSEALDLEGSVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
|||||
m790         250     260     270     280     290     300
IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI
|||||

a790.pep     310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
|||||
m790         310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTTT
51  TGGTTTGTTF TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

```

```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTGAG CGCGCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCAT ACAGAGGTT TTAAGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGGCGCGC CTGCGGTTT GCGGCCGAG CGGTCGATAA TGAGAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCGGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCG CGCCCAATG CAACCTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGACGAG GTGTGTCGGT GTCGGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

g791.pep

```

1 MVNYYSAMIK KILTTCTFGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTTRKF
151 NEVLLEYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNMMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDMKMPA VVLDVTKKKK VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPILLQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI VGGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT A VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

m791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGAG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
151 TACGAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GCGGATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGCAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

1268

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451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTC
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCGGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGGCTCAGC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTGCGTT ACGCGCAACG TATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACGC CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG CAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 CCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGACAGG AGCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLOH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPAKPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFED RGSSYRGAEN YIDLSKSEDEV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF ARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPKGK
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDRLRAQM QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKGG MKMPEGVVS NGEYYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

g791/m791 97.3% identity in 805 aa overlap

```
10 20 30 40 50 60
g791.pep MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
|||||
m791 MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
10 20 30 40 50 60

70 80 90 100 110 120
g791.pep SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
|||||
m791 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
70 80 90 100 110 120
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1269

g791.pep	130	140	150	160	170	180
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
g791.pep	190	200	210	220	230	240
	RAYGFASAAQIYFNKNVRDLTLAEAAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
g791.pep	250	260	270	280	290	300
	EKMITVQQORDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV					
m791	EKMITVQQORDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
g791.pep	310	320	330	340	350	360
	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
g791.pep	370	380	390	400	410	420
	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNGGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
	370	380	390	400	410	420
g791.pep	430	440	450	460	470	480
	AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLQALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
g791.pep	490	500	510	520	530	540
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
g791.pep	550	560	570	580	590	600
	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
g791.pep	610	620	630	640	650	660
	DRDGRRLRAQMPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
g791.pep	670	680	690	700	710	720
	TTNDNKDAWFVGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGKQKG					
m791	TTNDNKDAWFVGFNPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGKQKG					
	670	680	690	700	710	720
g791.pep	730	740	750	760	770	780
	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
g791.pep	790	800				
	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAT AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAATGCCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCCGT GACTATTTAT TCGGCGGATG GGGAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTC
601 ACTTTGGCGG AAGCCGCCAT GCTTGGCGGA CTGCCAAGG CTCGTCTGCG
651 CTATAATCCG ATTTGTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGCGTTTGA ATGAGGAAC GCATTACGAG CGGTTTGTTC GGAAAATCGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGCGCAGC GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGA AAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGCTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG CTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCCGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTTAT
1801 GACGAGACAG CAGGTTGCG CGCCAAATG CAACCTTTGG TGGCCGGGCA
1851 AATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GCGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGCGGCAAA GCGGACGCGC AGGCGGCGGA TGACGAAGTC GCGCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDLSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKREY
101 RHWGVDVWVG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEXYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 FEDRIRRGAV IRVKNNGGRW AVVQEPLLGQ ALVSLDARTG AVRALVGGYD
451 FHSKTFNRRAV QAMROPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGONAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKGG MKMPEGVVSS NGEYYMKERM VTDPLTLDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791 MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
10 20 30 40 50 60

70 80 90 100 110 120
a791.pep SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
|||||
m791 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
70 80 90 100 110 120

130 140 150 160 170 180
a791.pep GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
|||||
m791 GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
130 140 150 160 170 180

190 200 210 220 230 240
a791.pep RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
|||||
m791 RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
190 200 210 220 230 240

250 260 270 280 290 300
a791.pep EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
|||||
m791 EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
250 260 270 280 290 300

310 320 330 340 350 360
a791.pep RADHQKVATEALRKALRNFRGSSYRGAENYIDLKSEDEVEETVSQYLSGLYTVDKMPA
|||||
m791 RADHQKVATEALRKALRNFRGSSYRGAENYIDLKSEDEVEETVSQYLSGLYTVDKMPA
310 320 330 340 350 360

370 380 390 400 410 420
a791.pep VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
|||||
m791 VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
370 380 390 400 410 420

430 440 450 460 470 480
a791.pep AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
|||||
m791 AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
430 440 450 460 470 480

490 500 510 520 530 540
a791.pep KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
|||||
m791 KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
490 500 510 520 530 540

550 560 570 580 590 600
a791.pep GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
|||||
m791 GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
550 560 570 580 590 600

610 620 630 640 650 660
a791.pep DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG
|||||
m791 DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG
610 620 630 640 650 660

670 680 690 700 710 720
a791.pep TTNDNKDAWFGFNPDDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG
|||||
m791 TTNDNKDAWFGFNPDDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG
670 680 690 700 710 720

730 740 750 760 770 780
a791.pep MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGQAADDEV
|||||
m791 MKMPEGVVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLP	SNTGSKQQQL	DSLFX			
m791	RQDMQETPVLP	SNTGSKQQQL	DSLFX			
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CGggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAGAGGC GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtattTtTA TAAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaaaagc aaacggactg
701 attgttcag atattgaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAA KLTVLVPAPF
201 YYSDBPKSKR LRNKTNIIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTAC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAACA GCAGGCGGCA AAACCTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQAIR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIIVLK RMGSALPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALP	VGIFIFFNAYV	YVYGNIIITY	RAVAPHRTAF	MSMRMKQFEQ	EGRDVALDYR
m792	MFRIIKWLIALP	VGIFIFFNAYV	YVYGNIIITY	RAVAPHRTAF	MSMRMKQFEQ	EGRDVALDYR
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNL	LKKALIASD	VRFAGHGGFD	GDGIQNAIRR	NRNSGEVKAG	GSTISQQLAK

```
a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGCAC TGGATTACCG TGGATGCCCT ACAAAACGAT
151 GAAGTGC GCGC ATGTCGCAC TGGATTACCG TGGATGCCCT ACAAAACGAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGACGG CGGCTTCGAT TGGGGCGGCA TTCAAACAGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 CGGAAGAAGC GGGCATTACC CGGATGATGG AAGCCGTTAC CGACAAGAAG
451 AGGATTTTTT AACTGTATTT AAATCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA CGCGCGTCCC GGTATTTTTA TCAAAATACC CGCGCCGATC
551 TGACCAAACA GCAGGCGGGA AACGTGACG CCGCGCTCCC CGCCCGGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGGAT
701 GA
```

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIITY	RAVAPHGRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIAED	ARFAGHGFFD	WGGIQNAIRL
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYQIP	AAKLTQKQAA	KLTRVPAFL
201	YYADHPKSKR	LRKNTNIVLR	RMGSALFES	DTD*	

a792.pep	10	20	30	40	50	60
	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKKKALIASEDARFAGHGGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK					
m792	WMPYKRISTNLKKKALIASEDARFAGHGGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK					
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	NLFLNRSRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEASRYFYQIP					
m792	NLFLNRSRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEASRYFYQIP					
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	AAKLTQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDSTD					
m792	AAKLTQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDSTD					
	190	200	210	220	230	

q793.seq

1274

```
1 ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTGTTTGGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTGC CGGGACCGGC AGGGCAATAT
651 TGTTGGACAG TTGGACTCCC CGCGCAATAA AGCACCAGCA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGCG CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAAACG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCTCTTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGCGCGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAACCCGGC
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCAGGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCCGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```
1 MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51 TVTYNLFKEQ GDNRIVRTQA LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 DKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEEVL RDRGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM KXSNVGTSK LSAREFGAEM YDFYHELIG VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 ERQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVAKTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IAVTIDEPT AHGYGGGVVA
551 GPPFFKIMGG SLNILGISPT KPLTAAAVKT PS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```
1 ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTGTTTGGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGCG CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAAACG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
```

1275

```
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TCGGTTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAAATCC CCGTGTGAT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTAT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```
1 MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51 TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIVIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKALDAGKTDLNERLNTQPYKIGPSFVRDTHVYPSLDVRGIM
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KOAVAPOGKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKINGGS LNILGISPTK PLTAAVKTP S*
```

g793/m793 98.5% identity in 582 aa overlap

g793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
g793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
g793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
g793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
g793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
g793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	
g793.pep	370	380	390	400	410	420
m793	360	370	380	390	400	410

1276

```

      430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          |||||
m793      FGYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

      490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||||
m793      PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

      550      560      570      580
g793.pep  AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          |||||
m793      AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCGGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACTTTTT  GAAAGAACAG  GCGGACAACC  GGATTGTGCG
201 GACTCAAACA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGTGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCCGAGCT
351 TGTGATGTG  CCGGTTGATG  TTTTGAGGAA  CAAGCTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAGCCT  TGGGTTTGGA  AAACCTTTGT  TTTGAAAAAG  AATTAAAAACG
501 CCATTACCCG  ATGGCAACCC  TGTTGCACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTTGGAAC  TTTGCTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTTG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCCCCGAAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGCC  CTATGAAGAG
751 TTGAACAAGG  CGGTCGAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGGCCCGGC  CGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCCGGTTCC  GCAATCAAAC  CGTTTGTGAT
951 TCGGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCGGA  CCGTCTCCCG  TGCGCGATAC  CCATGTTTAC
1051 CCTCTTTGG  ATGTGCGCGG  CATCATGCAG  AAATCGTCCA  ACGTCGGCAC
1101 AAGCAAACCTG  TCTGCGCGTT  TCGGTGCCGA  AGAAATGTAT  GACTTCTATC
1151 ATGAGTTGGG  CATCGGTGTG  CGTATGCACT  CGGGCTTTCC  GGGCGAAACT
1201 GCAGGTTTGT  TGAGAAATG  GCGCAGGTGG  CGGCCTATCG  AACAGGCGAC
1251 GATGTCCTTC  GGTACGGCC  TGCAATTGAG  CCTGCTGCAA  TTGGCGCGCG
1301 CCTATACCGC  ACTGACGCAC  GACGGCGTTT  TACTGCCGGT  CAGCTTTGAA
1351 AAACAGCGCG  TTGCGCCGCA  AGGCAACGCG  ATATTCAAAG  AATCGACCGC
1401 GCGCGAGGTA  CGCAATCTGA  TGGTTTCCGT  AACCAGAGCG  GCGGCGACCG
1451 GTACGGCGGG  TGCGGTGGAC  GGTTCGATG  TCGGCGCGAA  AACCAGCACG
1501 GCGCGCAAGT  TCGTCAACGG  GCGTTATGCC  GACAACAAAC  ACATCGCTAC
1551 CTTTATCGGT  TTTGCCCGCG  CCAAAAATCC  CCGTGTGATT  GTGGCGGTAA
1601 CCATTGACGA  ACCGACTGCC  CACGGTTATT  ACGGCGGCGT  AGTGGCAGGG
1651 CCGCCCTTCA  AAAAAATTAT  GGGCGGCAGC  CTGAACATCT  TGGGCATTTT
1701 CCCGACCAAG  CCACTGACCG  CCGCAGCCGT  CAAAACACCG  TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR  MLPKEEQVK  PMTSNGRISF  VLMAIAVLFA  GLIARGLYLO
51  LTVTYNFKLQ  GDNRIVRTQ  LPATRGTVSD  RNGAVLALSA  PTESLFAVPK
101 EMKEMPAAQ  LERLSELVD  PVDVLRNKLE  QKGKSFIIK  RQLDPKVAEE
151 VKALGLENFV  FEKELKRHY  MGNLFHVG  FTDIDGKQ  GLELSLEDSL
201 HGEDGAEVVL  RDRQGNIVS  LDSPRNKAPK  NGKDIIISLD  QRIQTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRP  RADSEQRNR
301 AVTDMIEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPYKIG  PSPVRDTHVY
351 PSLDVRGIMQ  KSSNVGTSKL  SARFGAEMY  DFYHELIGIV  RMHSGFPGET
401 AGLLRNWRRW  RPIEQATMSF  GYGLQLSLLQ  LARAYTALH  DGVLLPVSE
451 KQAVAPQGR  IFKESTAREV  RNLMSVTEP  GGTGTAGAVD  GFDVGAKTGT
501 ARKFVNGRY  DNKHIATFIG  FAPAKNPRVI  VAVTIDEPTA  HGYYGGVVAG
551 PPFKKIMGGS  LNILGISPTK  PLTAAAVKTP  S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793						
	10	20	30	40	50	60
	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793						
	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793						
	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793						
	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
a793.pep	250	260	270	280	290	300
	ORIQTLAYEELNKAVEYHQAKAGTVVLDARTGEILALANTPAYDPNRPGRADSEQRRNR					
m793						
	250	260	270	280	290	300
	ORIQTLAYEELNKAVEYHQAKAGTVVLDARTGEILALANTPAYDPNRPGRADSEQRRNR					
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793						
	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793						
	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793						
	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793						
	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
a793.pep	550	560	570	580		
	HGYGGVVAGPPFFKKIMGGSNLGISPTKPLTAAAVKTPSX					
m793						
	550	560	570	580		
	HGYGGVVAGPPFFKKIMGGSNLGISPTKPLTAAAVKTPSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAAC AAGCCGGTCC GCCGCCCCGG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGCA
451 CCCGTTTCA ATCAGGAAAA CTGCTTGCC GTCCACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTGTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTGCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGCGCGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCF YVTDSPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRRLMD HSLWGEVGSF DHFEADSGSP
201 FMTFPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVMFMA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPVAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMMAQ LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGCGCC GCGGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTAT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCTCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTC ATCAGGAAAA CTTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTGCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV

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1279

101 NPASTMKLVLT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AOKQLREQGI LNITGHLMLD HSLWGEVGGP DDFEADSGSP
201 FMTFPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPECL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
401 RVTARMMAMQ LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTINNVRAL AGYWLGDKPM AVVVIINSGR AVSLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL					
m794	VRLNHFIMIAIIIVISPAKPARRHVSPTYPALPYNCFYVTDLPNMFPKTAASLLLLL					
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS					
m794	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
	70	80	90	100	110	120
g794.pep	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
m794	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
	70	80	90	100	110	120
g794.pep	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLD					
m794	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD					
	130	140	150	160	170	180
g794.pep	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLD					
m794	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD					
	130	140	150	160	170	180
g794.pep	HSLWGEVGGSPDHFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGGSPDDFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	HSLWGEVGGSPDHFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGGSPDDFEADSGSPFMTFPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNMKRSNLIARSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNMKRSNLIARSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNMKRSNLIARSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNMKRSNLIARSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
m794	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
	370	380	390	400	410	420
g794.pep	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
m794	GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMETAYFSPFA					
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDGLRNRFKQSGGLRLRLKTGLNNVRALAGYWLGDKPM AVVVIINSGR					
m794	QDFIDTLPIAGTDGLRNRFKQSGGLRLRLKTGLNNVRALAGYWLGDKPM AVVVIINSGR					
	430	440	450	460	470	480
g794.pep	QDFIDTLPIAGTDGLRNRFKQSGGLRLRLKTGLNNVRALAGYWLGDKPM AVVVIINSGR					
m794	QDFIDTLPIAGTDGLRNRFKQSGGLRLRLKTGLNNVRALAGYWLGDKPM AVVVIINSGR					
	430	440	450	460	470	480
g794.pep	AVSLPDLNDFVAKNIISGGDWLDKLMCKERRAX					
m794	AVSLPDLNDFVANNIISGGDWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTG CGCAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATGACC ACCGCTCGGA TGTCCCGCTC

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCGAG AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CCGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTTCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGCGCGCG AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGCGGAC GGCAACTGC CCGCGCTTTC
1101 CGAACAGGCA CCGTCTGCCG TCCGGCGTGA ACTTGCGTG TCGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACCG CTTATTTCAG
1251 CCCGTTTGA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCG GCGGTTTCCC
1451 TCGTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGCG
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFSK NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFFADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

```
10 20 30 40 50 60
a794.pep VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
|||||
m794 VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
10 20 30 40 50 60
70 80 90 100 110 120
a794.pep ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
|||||
m794 ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
70 80 90 100 110 120
130 140 150 160 170 180
a794.pep NYRWATEFSKNGTVNDGTLGDNLYWAGSGDPVFNQENLLAVQRQLREQGIRNITGHLMLD
|||||
m794 NYRWATEFSKNGTVNDGTLGDNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD
130 140 150 160 170 180
190 200 210 220 230 240
a794.pep HSLWGEVGSPPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAADSTDILTDPPLPHIFA
|||||
m794 HSLWGEVGSPPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
190 200 210 220 230 240
250 260 270 280 290 300
a794.pep QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFADELIRQSFT
|||||
m794 QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFADELIRQSFT
250 260 270 280 290 300
310 320 330 340 350 360
a794.pep NHWLLGGGRISDGIGISDTPGAQTLAVAHSKPMKEILTMNKRSNLIARSVFLKLGGD
```



This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

```
1 ATGCCGCTCTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT
51 TCAACGGGCG GATGcCGACC GCATCgG. TA CTTTGTCCAA TAATTGCGGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG
```

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGGCTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCCTGCCC GTTTTCTGCA
701 TTTGCCTGCA CCGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```
m900.pep
1  MPSETRQAEV RTASGSFORA DADRIXFYVQ *FACFFTRFR RACLQNLFDL
51  RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```
m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFORADADRIGYFVQXFACFFTRFRRAQLQNLFDLRRVGGQ
          ||||| ||||| | |||||:|:| | ||:| ||||| |||||: ||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRAQLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEFVDFKQWAFVGLFRL
          ||||:| :||| |||||:| | :| |||||:|:| ||||| |||||
g900      CVVAFQAQFCQFGVDFFRRKFFRLAPSQAVGKHLRKFRRFRRRGEFGFIDFKQRAVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFHFGQGEEFPEA
          ||||:| :||| ||||| |||||:| ||||| ||||| ||||| |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQEFDFVDFHFGQGEEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          ||||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
          190     200     210     220     230     240
```

1283

	240	250	260	270	280	290
m900.pep	HGGFVGMGAHVHQTLSGDAQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : :					
g900	NGGFVGVGAHVHQTLSGDAQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	: : : : :					
g900	LLLVAFFDDAVVIGEEEEFGFIEVLRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360
	360	370	380			
m900.pep	AASMPSEREKDVPIIPDLPTSSRQQTFPYX					
	: : : : :					
g900	TAAMPSEREKDAPIIPDLPTSSRQQTFPYX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

1	GAGGTTTCGGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCGCAT
51	CACGTACTTT	GCCCAATAAT	TCGCGTGCTT	CTTTACGCGC	TTTTTGCGCG
101	CCTGCCTGCA	AAATCTCTTC	GATTTGCGAA	GGGTCGGCGG	TCAGCTCGTT
151	GTAGCGTTTCG	CGCGGTTTCG	CGAGTTCGGC	GTTGATTTTC	GCCGCCAAAA
201	GTTTTTTTGC	CTCGCCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTCGTAAAT
251	TCTGCCGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATTT	CAAACAGAGG
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCGG	CTCTTTCATA	TTGGTGATGA
351	TTTTGTTGAC	CGATTTTGGG	GTTTTTTTGT	CGTTTTTCCA	AAGCGGAATG
401	GTGTTGCCGT	AGGATTTGGA	CATTTTGCGT	CCGTCCAAAC	CAACCAAGAG
451	TTGACGTTT	TCGTCGATTT	TCACTTCGGG	CAGTGTGAAG	AGTTCCCGBA
501	AGCGGTGGTT	GAAGCGGCCG	GCAATATCGC	GTGCCATTTC	AACGTGTTGG
551	ATTTGGTTCG	GACCGACTGG	AACTTCATGG	GCATTGAACA	TGAGAATGTC
601	GGCAGTCATG	AGGATAGGGT	AGCTGTACAA	ACCCATTTC	ACGCCGAAAT
651	CGGGGTCTTC	CTGCCCGTTT	TCCGCATTTG	CCTGCACGGC	GGCTTTGTAG
701	GCGTGGGCGC	GGTTCATCAA	ACCCTTGCGC	GTGATGCAGG	TCAGAAATCCA
751	GTTCAATTCC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC
801	GCTCGGGGTC	GAGTCCGCAG	GCAAGCCAAG	TGGCGGCAAC	GGCTTGGGTG
851	GATTGGTGAA	TCATCTCCGG	CTCGTGGCAT	TTGATGATAC	CGTGGTAATC
901	GGCGAGGAAG	AGGAAGGATT	CGGTATCAGG	GTTTTGCGCC	GCGCGGACGG
951	CGGGGCGGAT	AGCACCGACG	TAGTTGCCCA	GATCGGGGAT	GCCGGTGGTG
1001	GTTACGCCGG	TCAGAACTCG	TTTTTTGCTC	ATAAAAATGT	CCTTGCGGCA
1051	TCAATGCCGT	CTGAAAGGGA	AAAAGATGCG	CCGATTATAC	CCGATTTGCC
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA	

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

1	EVRTALGLFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNL	DLRRVGGQLV
51	VAFAFGEFG	VDERRQKFFC	LAPSQAVGKH	FRKFCRFR	GESFVDFKQR
101	AFVGLRLAR	LFHIGDDFVD	RFLGFFVFP	KRNGVAVGF	HFASVQTNQE
151	FDVFVDFHFG	QCEEFPEAVV	EAAGNIACHF	NVLDLVATDW	NFMGIEHENV
201	GSHEDRVAVQ	THFHAIEIGVF	LPVFRICLHG	GFVGVGAHVQ	TLGGDAQNP
251	VQFHHFGNVA	LTVEGGALGV	ESAGKPSGGN	GLGGLVNH	LVAFFDDTVVI
301	GEEEEFGIR	VLRRADGGAD	STDVVAQMRD	AGGGYAGQNS	FFAHKNVLA
351	SMPSEREKDA	PIIPDLPTS	SRQQTFFPY*		

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFRFRACLQNLFDLRRVGGQLVVA					
	: : : : :					
a900	EVRTALGLFQADTDRTITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

```
m900.pep      FARFGFEGVDFFRRQKFFGGFTPRQAVGKHFRKFHRRFRRRGESFVDFKQWAFVGLFRLARLF
|||          ||::|||          |||          |||          |||          |||
a900           FARFGFEGVDFFRRQKFFCLAPSQAVGKHFRKFRCRFRRRGESFVDFKQRAFVGLLRLARLF
60            70            80            90            100           110

m900.pep      HIGDDFDVDRFLGFFVVFPKRNGVAVGFGHFASVQTDOEFDVFIDFHFGQGEEFFEPAVVEA
|||          |||          |||          |||          |||          |||
a900           HIGDDFDVDRFLGFFVVFPKRNGVAVGFGHFASVQTNQOEFDFVDFHFGQCEEFFEPAVVEA
120           130           140           150           160           170

m900.pep      AGDVARHFVDLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGE
|||          |||          |||          |||          |||          |||
a900           AGNIACHFNVLDLVATDNFMGIEHNVSHEDRVAVQTHFAEIGVFLPVFRICLHGGE
180           190           200           210           220           230

m900.pep      VGMGAHVQTLGSDAGQNVPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
|||          |||          |||          |||          |||          |||
a900           VVGGAHVQTLGGDAGQNVPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
240           250           260           270           280           290

m900.pep      AFDDTVVIGEIEEEEGFGIEVLRRADGGADGADVVAQMRDAGGGYAGONSFFAHKNVLAASM
|||          |||          |||          |||          |||          |||
a900           AFDDTVVIGEIEEEEGFIRVLRRADGGADSTDVVAQMRDAGGGYAGONSFFAHKNVLAASM
300           310           320           330           340           350

m900.pep      PSEREKDVPPIIPDLPTSSRQQTFPYX
|||          |||          |||          |||          |||          |||
a900           PSEREKDAPIIPDLPTSSRQQTFPYX
360           370
```

```
g901.seq    not found yet
g901.pep    not found yet
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

m901.seq

```
1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCTTTTT CCATCACATT
51 GGTGCGCGGT TTGTTTACCG TATTaGyAG TGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 TTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGTTGCCG
301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGTATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGGG
601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGCCCA TGAAACCGTT
751 TACGGCTTGA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

1	MPDFSMSNLA	VAFSITLAAG	LFTVLXSGLV	MFSKTPNPRV	LSFGLAFAGG
51	AMVVVSLTEI	FSKSSEAEAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCGATT TTTGATGTC CAATTTGGCC GTTGCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
 401 CGCACAAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAT
 451 CCAGCAGTCG GGATGCCCTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCACC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGCCA TGAACCGTT
 751 TACGGCCTGA CAATGGGCAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFMSNLA VAFSITLAAG LFTVLXSG LVMFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	MPDFMSNLA VAFSITLAAG LFTVLGSG LVMFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVNPHE TLDAQDPSFQESKRRH					
a901	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVNPHE TLDAQDPSFQESKRRH					
	70	80	90	100	110	120
m901.pep	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	RSRKTWAC LLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
a901	RSRKTWAC LLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
	190	200	210	220	230	240
m901.pep	KRYSDGHETVYGLTTGMAVIAVSLVLFHFX					
a901	KRYSDGHETVYGLTMGMAVIAVSLVLFHFX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCGCCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCGATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTTCAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TCGTGcgcG CGcgcccgtg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtggttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGSAFQCQTQ
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAI F GDFGDGGQVL
201 IVVVPQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDL RPE SDVVT RIRH LFGVAAGNLH GNDAAFIGKI TAVQFGSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACGCGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGCAGAT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCGCCGAC
651 GGACGACGCG TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCCCAT CCGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQGR
101 QNTVFGIMFQ IAEFPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHORATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTTCLFAVGHF				
g902	MPSEPERRHGNTALPFPPIAARPTVGFSGKPKITGKCVLRRRIVQAVDFTPRLFAVGHF				
	10	20	30	40	50
	60				
m902.pep	70	80	90	100	110
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSG GAFQCQTQGR RQNTVFGIMFQIAEEPRPA				
g902	ADVPAYVFACDAHTDGLTIKRVHGADVQNGGSAFCQTQGRXNAVFGIMLQIAEKPRPA				
	70	80	90	100	110
	120				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVD PDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	LRAAPYHNAVGGGLFEDGGGFLRRSDVAVD PGRDVQTAFLGDEFVTRLAFVHLRARAPV				
	130	140	150	160	170
	180				
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHORATGL				
g902	NGKGGNAIFGDFGDDGQVLIVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHORATGL				
	190	200	210	220	230
	240				
m902.pep	240	250	260	270	280
	DIADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	DVAHFLGGAHIDVDDL RPESDVVTRRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
	250	260	270	280	290
	300				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNAHR RRCDCGVVDKIAADVHNGSAFQKSTPLY				
g902	ERRIAGQHFAHRPTCAKRPTAEAGFVGNAHR RRCDCGVVDKITADVHNGPAFQKSAPLY				
	310	320	330	340	350
	360				
m902.pep	IFX				
g902	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

```

```
101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAAGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG CGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFQCQTQRR
101 *NTVFGVMFQ IAEEPRSA LR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *
```

m902/a902 94.7% identity in 360 aa overlap

m902.pep	10	20	30	40	50	60
	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD					
a902	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD					
	10	20	30	40	50	60
m902.pep	70	80	90	100	110	120
	VPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQCQTQGRRQNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDAHTGGVAVKRVHGSDDVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRSA LR					
	70	80	90	100	110	120
m902.pep	130	140	150	160	170	180
	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	190	200	210	220	230	240
	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGNAAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	250	260	270	280	290	300
	ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	310	320	330	340	350	360
	RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF					

```

a902      |||||
          RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep   X
           |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattc gatgaggCAA GCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTCaa ccaTGCTTG tgcAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAAC GTCTGTGCTG CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAAATTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTTCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTCCGAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRs
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNL LNLRLDLEOGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVQ WRXRLLPYCV SVGMDSNGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSIIIDAEI TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFPQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKVVTFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51 CCGTTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

```

151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCCTCGTTT
501 GCCGAGTGT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAAGT TACAGCGTGC ATTATTCCGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGAC ACGCCAAACC TATAAATCA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGCTTTAC AAACCGCGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCCAAA GGCTTTTACA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEERKRDG KSAEGSISAF NKNFPLYRNK
151 ILNLRDVEQG LENLRLRPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL AHKTDLTDAT
251 GTETESGSRs YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |:::| |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90      100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPQNMDSGIL KLRVSAGEIG
          : : | | : | | : : : : : : : : : : : : : : : :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRI LAAPQDLNSGKLQTLMPGYLR
          40      50      60      70      80      90

```

1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQUIPSE					
g903	SIRIDRSNDDQTHAGRIAFAFQNKFPTRSNDDLNLRLDLEQGLNLRKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQNK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDFVYSYGR					
g903	REPNSQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFVYNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTDTGTETESGSRYSVHYSVPVKWLFNFHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSGVMKLTROTQYKYIDDAEIEVQRRRSAGWEAELRHRAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDDAELTVQRRKTTGWLAEELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMQRQMPAPEENGDDILPGTSRMKIITASLDAAAPFXLGKQOFF					
g903	IGRSTADFKLYKHGTGMKDALARPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPLTSQDKLAIGGHHTVIRGFDGEMSLPAERGWIWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
g903	TGFQVGYSEFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

```

1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTAGATGA TAAGACGGCG
151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATTGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAACCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT

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1292

```
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTGGT
801 GCCCCGAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTAGT
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```
1 MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAPF MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

m903/a903 98.4% identity in 547 aa overlap

```
10 20 30 40 50 60
m903.pep MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
a903 MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTARKFSFLPSVL
10 20 30 40 50 60
70 80 90 100 110 120
m903.pep MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
a903 MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
70 80 90 100 110 120
130 140 150 160 170 180
m903.pep DIRYEEKRDG KSAEGSISAF NNFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQUIPSE
a903 DIRYEEKRDG KSAEGSISAF NNFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQUIPSE
130 140 150 160 170 180
190 200 210 220 230 240
m903.pep EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL
a903 EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL
190 200 210 220 230 240
250 260 270 280 290 300
m903.pep AHKTDLTDAT GTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
a903 VHKTDLTDAT GTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ
```


1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKT	SVGMKLWTRQTYKYIDDAE	IEVQRRRSAGWEAELRH	RAYLN		
a903	YQSSLAERMLWRNRFHKT	SVGMKLWTRQTYKYIDDAE	IEVQRRRSAGWEAELRH	RAYLN		
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRG	TGMRSMPAPEENG	DILPGTSRMKIITAS	LDAAAPFXLGKQ	QFFYA	
a903	RWQLDGKLSYKRG	TGMRSMPAPEENG	GGTIPGTSRMKIITAG	LDAAAPFMLGKQ	QFFYA	
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDK	SIGSRYTVRGFDGEQ	SLFGERGFYWQNTLT	WYFHPNHQFYLG		
a903	TAIQAQWNKTPLVAQDK	SIGSRYTVXGFDGEQ	SLFGERGFYWQNTLT	WYFHPNHQFYLG		
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSG	KQLMGAVVGRGGHKV	GMFAYDLFAGKPLHK	PKGFQTTNTVYG		
a903	ADYGRVSGESAQYVSG	KQLMGAVVGRGGHKV	GMFAYDLFAGKPLHK	PKGFQTTNTVYG		
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGAGACT TCTTCAATCC GTTTCAAATA TGCTTTGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCG CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATAACGGAA ATGCGTTTGA TTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGGCC GCAGCGGCGC GCGCGGCCG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTTCGTTCAA CACGCGgggac acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTGGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatattA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRRFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

```

51  AGHGFVNRF  GFHRTARQ  DVGFAAAWQF  VADADIDGFN  AVHYIEFGNA
101 HTGNAVLDLG  AFQGGGKPA  AAARAAGYRT  EFVSALRQTC  AYFVEQFGRE
151 RARTDARGIG  FDDAQNIQH  LRTYARACRS  RAGETVGRGN  EGVSADVVDQ
201 QRTLRAFQKQ  FFAVFVFFVQ  HAGHVGNHRR  NARRDFFDNR  HHVFRFNRSR
251 VMQVLELDV  IGKDGIFFT  QFFRMQQIGG  ANGAACHFVF  VGRADAAAGR
301 ADFAFAARCF  AGLVERDVVR  QDQRAGRRDF  QTAFDVFHAC  RVQLVDFAAQ
351 GFGGNDNART  DEAIQSFVQD  TARNQAQNGF  FAADDQGMAR  IVAALEAHDA
401 AGFRQPVND  FTFTLVAPLC  ADYNNIFSHS  HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904.seq

```

1  ATGATGCAGC  ACAATCGTTT  CTTCTCGGTC  GGGGCCGgTG  GAGACGATGG
51  CGACCGGCGC  GCCGCAGACT  TCTTCAATCC  GTTTCAAATA  TGCTTTGGCG
101 TTTTCGGGCA  ATGCGCCGTA  GTCCTTCACG  CCGAAAGTGG  ATTCGCGCCA
151 GCCGGGCATG  GTTTCGTAAA  TCGGCTTGCA  GGTTCACACC  GCATCGGAAC
201 CGCAAGGCAG  GATGTCGGTT  TTGCCGCCGT  CGGGCAATTC  ATAGCCGACG
251 CAGATATTGA  TGGTTCAAC  GCCGTCCATT  ACATCGAGTT  TAGTAATACA
301 CATACCGGAA  ATGCCGTTGA  TTTGGATGGA  GCGTTTCAGG  GCGGCGGCAT
351 CAAACCAGCC  GCAGCGCGCT  GCGCGTCCGG  TTACCGAACC  GAATTCGTGT
401 CCGCGTCTCG  CCAAACCTAC  GCCTACTTCG  TCGAACCAAT  CGGTCGGGAA
451 CGGGCCCCGA  CCGACGCGCG  TGGTATAGGC  TTTGACGATG  CCAAAACAT
501 AATCCAGCAT  TTGAGGACCT  ACGCCCGCGC  CTGCCGAAGC  TCGCCCCGCC
551 AGACAGTTGG  ACGAGGTAAC  GAAGGGATAA  GTGCCGTAGT  CGATGTCCAA
601 CAACGCACCT  TGC CGCCTT  CAAACAGCAG  TTTTTCGCCG  TTTTGTGTTT
651 TCTCGTTCAA  CACGCGGGAC  ACGTCGGTAA  TCATCGGCGC  AATGCGCGGC
701 GCGACTTTTT  CGATAACCGC  CATCACGTCT  TCCGCTTTAA  CCGGCTCGGC
751 ATTGTGCAGA  TGTTCAGTT  GGACATTGTA  ATAGGCAAGG  ACGGCATCCA
801 GTTTTTTCAG  CAGTTTCTCA  GGATGCAGCA  AATCGGCGGC  GCGAATGGCG
851 CGGCGTGCCA  CTTTGTCTTC  GTAGGCAGGG  CCGATGCCGC  GGCCGTCGT
901 GCCGATTTTG  CCTTTGCCGC  GCG.ATcTTC  GCGGGCTTGG  TCGAGCGCGA
951 TGTGGTAAGG  CAGGATCAGC  GGGCAGGTCG  GCGCGATTTT  CAGACGGCCT
1001 TCGACGTTTT  TCACGCCTGC  CCGCTTCAAC  TCGTCGATTT  CGCCCAACAG
1051 GGCTTCGGGG  GAGACGACAA  CGCCCGAACC  GATGAAGCAG  TCCAACTTT
1101 CATGCAGGAT  GCCGCTCGGA  ATCAGGCGCA  AAATGGTTTT  TTTGCCGCCG
1151 ACAACCAAGG  TATGGCCCCG  ATTGTGGCCG  CCTTGAAGC  GCACCaCGCC
1201 GCCGGCTTCT  TCCGCCAGCC  AGTCAACGAT  TTTACCTTTA  CCCTCGTCGC
1251 CCCACTGTGC  GCCGATTAsT  ACAACATTTT  TAGCCATAGC  CATATAACCT
1301 ATCGATATTA  A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pep

```

1  MMQHNRF  FSV  GAGGDDGDRR  AADFFNPFI  CFGVFGQCAV  VLHAESGFAP
51  AGHGFVNRL  GFHRIGTARQ  DVGFAAVGQF  IADADIDGFN  AVHYIEFSNT
101 HTGNAVLDLG  AFQGGGKPA  AAACASGYRT  EFVSALRQTC  AYFVEQFGRE
151 RARTDARGIG  FDDAQNIQH  LRTYARACRS  CARQTVGRGN  EGISAVVDVQ
201 QRTLRAFQKQ  FFAVFVFLVQ  HAGHVGNHRR  NARRDFFDNR  HHVFRFNRLG
251 IVQMLQLDIV  IGKDGIFFT  QFXRMQQIGG  ANGAACHFVF  VGRADAAAGR
301 ADFAFAAXIF  AGLVERDVVR  QDQRAGRRDF  QTAFDVFHAC  RVQLVDFAAQ
351 GFGGDDNART  DEAVQTFMQD  AARNQAQNGF  FAADNQGMR  IVAALEAHHA
401 AGFRQPVND  FTFTLVAPLC  ADXYNIFSHS  HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

```

          10      20      30      40      50      60
m904.pep  MMQHNRF  FSVGAGGDDGDRRAADFFNPFI  CFGVFGQCAVVLHAESGFAPAGHGFVNRLA
          |||:|||||:|||||:|||||:|||||:  ||:|:|:|:|  |||:|||||:|
g904      MMQHNRF  FAVGAGGDDGDRRAADFFNPFI  CFGIGRQCVVAFHADS RFAPAGHGFVNRLA
          10      20      30      40      50      60
          70      80      90      100     110     120

```

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m904 . pep	GFHRIGTARQDVGF	AAVGGQFIADAD	IDGFNAVHYIEFS	NTHTGNAVDLDGA	FQGGGIKPA
g904	GFHRIRTARQDVGF	AAAWQFVADAD	IDGFNAVHYIEFG	NAHTGNAVDLDGA	FQGGGIKPA
	70	80	90	100	110 120
m904 . pep	AAACASGYRTEFVS	AFCQTYAYFVEQ	FGREARTDARGIG	FDDAQNI IQHLR	TYARACRS
g904	AAARAAGYRTEFVS	ALRQTCAYFVEQ	FGREARTDARGIG	FDDAQNI IQHLR	TYARACRS
	130	140	150	160	170 180
m904 . pep	CARQTVGRGNEGIS	AVVDVQORTLRAF	KQQFFAVFVFLVQ	HAGHVGNHRRNAR	DDFFDNR
g904	RAGETVGRGNEGVS	AVVDVQORTLRAF	KQQFFAVFVFFVQ	HAGHVGNHRRNAR	DDFFDNR
	190	200	210	220	230 240
m904 . pep	HHVFRFNRLGIVQ	MLQLDIVIGKDG	IQFFTFQFXRMQ	QIGGANGAACHFV	FVGRADAAAGR
g904	HHVFRFNRSQVLM	QVLELDVIGKDG	IQFFTFQFFRMQ	QIGGANGAACHFV	FVGRADAAAGR
	250	260	270	280	290 300
m904 . pep	ADFAFAARIFAGL	VERDVVRQDORAG	RRDFQTAFDVFHA	CRVQLVDFDAQQ	GFGGDDNART
g904	ADFAFAARCFAGL	VERDVVRQDORAG	RRDFQTAFDVFHA	CRVQLVDFDAQQ	GFGGDDNART
	310	320	330	340	350 360
m904 . pep	DEAVQTFMQDAARN	QAQNGFFAADNQ	GMARIVAALAHHA	AGFFRQPVNDFT	TFTLVAPLC
g904	DEAIQSFVQDTARN	QAQNGFFAADNQ	GMARIVAALAHDA	AGFFRQPVNDFT	TFTLVAPLC
	370	380	390	400	410 420
m904 . pep	ADXYNIFSHSHIT	YRYX			
g904	ADYYNIFSHSHIT	YRYX			
	430				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTCTTG	CCAAACCTGC	TCCGACTTCG	TGCAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCCAGCG	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGT TTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGAAGC GCACCACGCC
1201 TCCGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904 . pep

```

1 MMQHNRRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHR LG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQOIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYNNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904 . pep	10	20	30	40	50	60
	MMQHNRRFFSVGAGGDDGDRRAADFFNPFI CFIGRXCVVAFHAESGFAPAGHG FVNRLA					
a904	MMQHNRRFFAVGAGGDDGDRRTADFFNPFI CFIGRXCVVAFHAESGFAPTGHG FVNRLA					
	10	20	30	40	50	60
m904 . pep	70	80	90	100	110	120
	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA					
a904	GFYRIRAAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTHGTGNAVDLDGAFQGGGIKPA					
	70	80	90	100	110	120
m904 . pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRE RARTDARGIGFDDAQNIIQHLRTYARACRS					
a904	AAACASGYRTEFVSAFCQTCSD FVEQFGRE RARTDARGIGFDDAQNIIQHLRAYARACRS					
	130	140	150	160	170	180
m904 . pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQRTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	RAGEAVGRSNEGVSAVVDVQRTLRAFQKQFFAVFVFFVQHAGHVGNNRRNARRDFFDNR					
	190	200	210	220	230	240
m904 . pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQOIGGANGAACHFVFVGRADAAAGR					
a904	HHVFRFHR LGIVQMLQLDVVISKDGIOFFTQFFRMQOIGGANGAACHFVFVGRADAAAGR					
	250	260	270	280	290	300
m904 . pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART					
a904	ADFAFAARCF SGLVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART					
	310	320	330	340	350	360
m904 . pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

430

```

m904.pep    ADXYNIFSHSHITYRYX
             || ||||| ||||| |||
a904        ADYYNIFSHSHITXRYX
             430

```

g906.seq not found yet

g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
  1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101  TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151  CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201  CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251  GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAACAAA
301  AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
  1  MKYIVSISLA MGLAACSFEGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101  KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
  1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
 51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101  CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151  TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201  GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGTC
251  CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301  AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351  aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
  1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
 51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101  SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
  1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
 51  GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101  CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151  TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201  GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGTC
251  CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301  AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351  AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCTGA
401  TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAACC GGCGCACAAc
451  CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501  TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551  ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601  CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
  1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
 51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101  SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

```

151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGLSGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	:	:	:	:	:	:
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
g907.pep	RARIIS					
m907	ROYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGGCG
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTGCGCA	GCATAAATCC	GCCGAGGCTG	GTGTTCGACA	ATCCGAAAGA
201	GGGCGAGCGT	TGGCTGTCCG	CGATGTCTGC	TCGGTTGGCA	AGGTTCTGTC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGG	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTTGG	AAAAACTACA	TCGGCAAACC	GGCGCACAAAC
451	CTGTTTCGACA	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCCGTTTA
551	ACGGTAGCCT	CGGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAQREETL	ADDVASVMRS
51	SVGSINPPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	ROYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHRYN	LEKGNIVRAL	ARFNGLSGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	:	:	:	:	:	:
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
m907.pep	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
a907	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
m907.pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatt TTagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPRIREQVK PDSIVYTDCY RSYDVLVDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGCG AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPRIREQVK PDSIFYTDCY RSYDVLVDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g908.pep	MXKSRLSRYKQ	QNKLI	GLFVAGVT	ARTAAELV	GINKNTAAY	DFHRLRLXLI
	QNGPHLEMF					

1300

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAAYYFHLRLLLIYQNSPHLEMF	10	20	30	40	50	60
		70	80	90	100	110	120
g908.pep	GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK						
m908	GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK	70	80	90	100	110	120
		130	140	150	160		
g908.pep	PDSIVYTDCYRSYDVLVDVSEFSHFSAETSFSYQSQHTFCRTTKPYX						
m908	PDSIFYTDCYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRTTKPYX	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

a908.seq

```
1 ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51 ATTTGTGCGA GGTGTAAGTG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAC GCAAAGGCCA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCCCTA TTATCCGTAG
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCCGCAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A
```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

a908.pep

1	MRKSRLSQYK	QNKLIELFVA	GVTARTAAEL	VGVNKNTAAY	YFHRLRLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKGR	GAAGKVAVFG	LLKRNGKVYT
101	VTVNTQTAT	LFPIIREQVK	PDSIVYTDY	RSYDVLVDRE	FSHFSFAETS
151	FSYQSQTFC	RTTKPY*			

m908/a908 98.2% identity in 166 aa overlap

```

m908.pep      10      20      30      40      50      60
MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMFD
|||||:|||||
a908          10      20      30      40      50      60
MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMFD

m908.pep      70      80      90     100     110     120
GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPIIREQVK
|||||
a908          70      80      90     100     110     120
GEVEADESYFGGQQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPIIREQVK

m908.pep      130     140     150     160
PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
|||||
a908          130     140     150     160
PDSIVYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```

1  atgcgtaaaa ccgtacttat cCTgaccatc tccgccgccc ttttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```



```

151 aaaaagggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
201 caacccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acggggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	SKKVDCDEYGG
	10	20	30	40	50	60

	70	80	90
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNRX
	:		: : :
g909	ERRAVLRNQK	RGKPTRRAA	TLGKPSFRARDGGGRVNRAETGEGKRSAR
	70	80	90 100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILIMT AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
a909	MRKTFILIMT	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLNAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
m910	MKKLLLAADVSLNAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATGTGTGTTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
 51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVYD
	:	:	:	:	:	:
a910	MKKLLLV	AVVSLS	AATAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYKD	GREYDIV	LSYPDL	KIIKE	QLDRX
	:	:	:	:	:	:
a910	GKPVLE	VEAYKD	GREYDIV	LSYPDL	KIIKE	QLDRX
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
 1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCTTGATCGG
 51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT
 101 TCGGCGGTTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCCG
 201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
 351 CGGCGATACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCACTT
 401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
 451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
 1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCCTGATTGG
 51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
 101 TCGGCGGTTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCCG
 201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
 351 CGGCGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCACTT
 401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTCGCC
 451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
 1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGS DKTYAVYADFGDIGGLKVNAPVK
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGS DKTYAVYADFGDIGGLKVNAPVK
           10      20      30      40      50      60

           70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
m911      SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
           70      80      90      100     110     120

           130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKA AEX
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKA AEX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
  1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCCTGATTGG
 51  CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCG CGTGGCCGCG GGTGCGGCGT
101  TCGGCGGTTTC GGACAAAAC TACGCCGTTT ATGCCGATT TCCTGACATC
151  GGCGGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201  GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251  GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301  ATCCTGACTT CGGACTTTT GGGCAGCAG TACATCGGCG TGCAGCAGGG
351  CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCA GTT
401  CTGCAATGGT TCTGGA AATC TCGGCA AATT CATGAC GAGTTT TGCC
451  GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
  1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101  ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151  EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGS DKTYAVYADFGDIGGLKVNAPVK
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGGS DKTYAVYADFGDIGGLKVNAPVK
           10      20      30      40      50      60

           70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
a911      SAGVLVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
           70      80      90      100     110     120

           130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKA AEX
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKA AEX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
  1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
 51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101  ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

151	CGCCCAAAAG	CCGAAGCCTA	TGCGGTTCCC	TATTTGATT	TCCAACGTAT
201	GACCGCATTG	GCGGTGCGCA	ACCCTTGGCG	TACCGCGTCC	GACGCGCAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCAGCATGC	TGAAATTCAA	AAACGCGACC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAGGGCGGCA	AGGAAATCGT	CGTCCGTGCC	GAAGTCGGCA
401	TCCCGGCTCA	GAAGCCCGTC	AATATGGACT	TTACCACCTA	CCAAAGCGGC
451	GGCAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCACGA	GCCTGGTTAC
501	CGTGTACCGC	AACCAATTGC	GCGAAATCAT	CAAGGCAAAA	GGCATCGACG
551	GGCTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAAATA	A

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

g912.pcp

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYTS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI I KAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTTGAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTTCGATT	TCCAACGTAT
201	GACCCGACATG	CGGGTCGGCA	ACCTTGGCGC	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
451	GGTAAATACC	GTACCTACCA	CGTCGCCATC	GAAGGCGCGA	GCCTGGTTAC
501	CGTGTACCGC	AACCAATTAG	GCGAAATTAT	CAAAGCGAAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAAATA	A

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

m912.pcp

```

1  MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRTAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEIISK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

from *N. gonorrhoeae*:

g912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP					
m912	: : : : : : : : : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFDIFORMTALAVGNPWRTASDAQQALAKEFOTLLIRTYSGMTLKFKNATVNVKDNPIVN					
m912	: : : : : : : : : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIIVRAEVGIPGQKPVMNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEIIKAK					
m912	: : : : : : : : : : : : : : :					
	130	140	150	160	170	180

g912.pep 190 GIDGLIAELKAKNGGKX

1306

m912

|||||
GVDGLIAELKAKNGGKX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq
1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGATTCCC TATTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCCTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep
1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRONATQVLS ILKSGDANTA
51 RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
101 GTMLKLKNNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLTVYR NQFGEIIRAK GVDGLIAELK AKNGSK*

m912/a912 98.0% identity in 196 aa overlap

m912.pep	10	20	30	40	50	60
	MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRONATQVLSILKSGDANTARQKAEAYAIP					
m912.pep	70	80	90	100	110	120
	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNNANVNVKDNPIVN					
a912	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNNANVNVKDNPIVN					
m912.pep	130	140	150	160	170	180
	KGGKEIIVRAEVEGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEIIRAK					
a912	KGGKEIIVRAEVEGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEIIRAK					
m912.pep	190					
	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq
1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCAGAAACCC GCCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCGGCGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA
251 TCTTGCCTTT GGAcatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg
351 cgcgcttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

g913.pcp

m913.seq

m913.pcp

g913/m913

BNSDOCID: <WO_9957280A2 | >

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAEAGAAEPVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAEAGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

a913.seq

1	ATGAAAAAAA	CGGCCTATGC	CTTCCTCCTG	CTGATCGGGT	TCGCTTCCGC
51	CCCTGCATTT	GCCGAAACCC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTTT	CAAATTC AAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCCCT
151	GCCGCGCGCG	GCTACCGCAA	AGTTGCGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTTT	TTTAACAACC	TGTGCGACGT	GGTCAGCTTC	GGCAGCAATA
251	TCTTGCGCTT	AGACATCAAA	CGCGCAAGCG	AAGACCTTGT	CCGCGTCGGT
301	ATCAACACCA	CTTTCGGTTT	GGGCGGGCTT	ATCGACATCG	CCGGCGCGGG
351	CGGCATTCCC	GACAATAAAA	ACACCTTGGG	CGACACGTTT	GCTTCGTGGG
401	GATGGAAAAA	CAGCAATTAT	TTCGTGTTGC	CCGTCTTAGG	GCCGTCCACC
451	GTCCGCGACG	CGCTCGGCAC	GGGTATTACC	TCCGTTTATT	CGCCCAAGAA
501	TATCGTCTTC	CGCACCCCTG	TCGGACGCTG	GGGCACGACT	GCCGTATCCG
551	CCGTCAGTAC	GCGCGAAGGC	CTGCTCGATT	TGACCGACAG	TCTGGACGAA
601	GCCGCCATCG	ACAAATACAG	CTACACGCGC	GACCTCTATA	TGAAAGTCCG
651	TGCGCGGCAG	ACCGGTGCAA	CACCTGCCGA	AGGTACGGAA	GATAACATCG
701	ACATCGACGA	ATTGGTCGAA	AGTGCCGAAA	CCGGCGCGGC	GGAAACTGCC
751	GTTCAAGAAG	ATTCCGTATC	CGAAACACAG	GCAGAAGCAG	CAGGGGAAGC
801	CGAAACGCAA	CCTGGAACAC	AACCTGGAAC	ACAACCTTAA	

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

a913.pep

1	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP
51	AARGYRKVAP	KPVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG
101	INTTFGLGGL	IDIAGAGGIP	DNKNTLGDTF	ASWGWKNSNY	FVLPVLGPST
151	VRDALGTGIT	SVYSPKNIVE	RTPVGRWGTT	AVSAVSTREG	LLDLTDSLDE
201	AAIDKYSYTR	DLYMKVRARQ	TGATPAEGTE	DNIDIDELVE	SAETGAAETA
251	VQEDSVSETQ	AEAAGEAETQ	PGTQPGTQP*		

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAGVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGLIDIAGAGGIP					
a913	KPVRAGVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTGCA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLW
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTGCA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTTCGTAGG CTTTCGACGAT TTTTTCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTCGC CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGTGTTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMRVNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAPADRISDLRLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAPADRIGDLRLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALECSQSCSADSXASTIFCTRGCRRTSSPVKWKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPNDLMFLGRSIWLSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNDLMFLGRSIWLSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTCT
451 TAGGCTTCGA CGATTTTGTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG
551 CATCTTTTAA TCCCGATTGT ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGG TGTTTTGC GC TCAGGAGG ATGATGTATG
701 CGCCGTTGAG CGTCCTGCCG CGCATATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLRLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPNDL MFLGRSIWLV
201 SPVMTAFAPK PMRVNIFIC SGVVFCASSR MMYAPLSVLP RI*
  
```

m914/a914 98.4% identity in 244 aa overlap

```

      10      20      30      40      50      60
m914.pep  MKKCILGILTACAAMPAFADRIDGLEARLAQLEHRVAVLES GGNTVKIDLF GSNSTMYVC
          |||||
a914      MKKCILGILTACAAMPAFADRIDGLEARLAQLEHRVAVLES GSNSTVKIDLF GSNSTMYVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m914.pep  SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD
          |||||
a914      SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--
      70      80      90     100     110

      130     140     150     160     170     180
m914.pep  TELGFRICFSLPDFPCIGFQTALEQCSCSAD SXASTIFCTKGCRTTSSPVKVKYSPSTL
          |||||
a914      TELGFRICFSLPDFPCIGFQTALEQCSCSAD SXASTIFCTKGCRTTSSPVKVKYSPSTL
      120     130     140     150     160     170

      190     200     210     220     230     240
m914.pep  CSFSRASFNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
          |||||
a914      CSFSRASFNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
      180     190     200     210     220     230

m914.pep  LPRIX
          ||||
a914      LPRIX
          240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGCK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```
m915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```
m915/g915

      10      20      30      40      50      60
m915.pep  MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep  DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS
          70      80      90     100     110     120

      130     140     150     160
m915.pep  GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g915      GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX
          130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```
a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGCCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCC TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```
a915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m915/a915 99.4% identity in 164 aa overlap

```
m915.pep  MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a915      MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep  DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccact cgcCGTCctg actgctTtgc tgcttgccagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCACTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNK IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCAACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
 801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACCTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
 1101 CAGTGGCAG GATGTGAAGG CGGGGAATA A

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCTVTIGF
 251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNAFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNAFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDI REATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDI REATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCTVTIGFGGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCTVTIGFGGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

370

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m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTGAAAATT TACAACCTGGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCTG
 251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
 401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
 501 GGATTGCGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCG
 701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
 751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
 801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLNIAKRR AEEAGGKEKI RVMPMPKEGVG IWVDSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPE TVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPE TVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLSAAAEIYPMVLNVLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLSAAAEIYPMVLNVLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep						

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a917      QCGISYLDAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           |||||||
a917      RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           |||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGTCAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGCTAT TACGAACCG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCGC ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCCT
801 GAAAACCCCg tccggcaaat acatCCGCaT cggaTaccgc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGVTGY YEPVLKGDGR
151 RTERARFPPI GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSLFPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPOR LAEVLQNPNS YIFFRELAGS GNEGPGVAGL
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```


This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:
m919.pep

1	<u>MKKYLFRAAL</u>	<u>YGIAAAILAA</u>	<u>CQSKSIQTFP</u>	<u>QPDTSVINGP</u>	<u>DRPVGIPDPA</u>
51	<u>GTTVGGGGAV</u>	<u>YTVVPHLSLP</u>	<u>HWAAQDFAKS</u>	<u>LQSFRLGCAN</u>	<u>LKNRQGWQDV</u>
101	<u>CAQAFQTPVH</u>	<u>SFOAQOFFER</u>	<u>YFTPWQVAGN</u>	<u>GSLAGTVTGY</u>	<u>YEPVLKGDDR</u>
151	<u>RTAQARFPIY</u>	<u>GIPDDFISVP</u>	<u>LPAGLRSGKA</u>	<u>LVRIRQTGKN</u>	<u>SGTIDNTGGT</u>
201	<u>HTADLSRFPI</u>	<u>TARTTAIKGR</u>	<u>FEGSRFLPYH</u>	<u>TRNQINGGAL</u>	<u>DGKAPILGYA</u>
251	<u>EDPVELFMFH</u>	<u>IQSGRLKTP</u>	<u>SGKYIRIGYA</u>	<u>DKNEHPYVSI</u>	<u>GRYMADKGYL</u>
301	<u>KLQQTSMQGI</u>	<u>KSYMRQNPQR</u>	<u>LAEVLGQNPS</u>	<u>YIFFRELAGS</u>	<u>SDNGPVGALG</u>
351	<u>TPLMGEYAGA</u>	<u>VDRHYITLGA</u>	<u>PLFVATAHPV</u>	<u>TRKALNR LIM</u>	<u>AQDTGSAIKG</u>
401	<u>AVRVDYFWGY</u>	<u>GDEAGELAGK</u>	<u>QKTTGYVWQL</u>	<u>LPNGMKPEYR</u>	<u>P*</u>

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQP	DTSVINGPDRPVGIPDPAGTTVGGGGAV				
	: : : : :					
g919	MKKHLLRSALYGIAAAAILAACQSR	SRIQTFFQP	DTSVINGPDRPAGIPDPAGTTVAGGGAV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
	: :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

```

a919.seq
1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGCCCGG GACCGGCCGG TCGGCATCCG CGACCCCGCC
151 GGAACGACGG TCGCGCGCGG CGGGCCGTTG TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT GCCAAAAGC TGCACATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTCCAG CAAAACAGTT
351 TTTGAACGC TATTTACGC CGTGCCAGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG GCAGCAGAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCGTCCTCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGACAGC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC CACGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAAGTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGCGCGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCGCTGTA TGGCGGAGTA CGCCGCGGCA CTCGACCGG ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAA

```

1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
 1201 GCGGTGCGCG TGGATTATT TTGGGGATAC GCGGACGAAG CCGGCGAACT
 1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
 1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:
 a919.pep

1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
 51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
 101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
 151 RTAQAQRFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
 201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
 251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
 301 KLGQTSMOGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
 351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
 401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap

	10	20	30	40	50	60
m919.pep	MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
a919	MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
a919	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER					
	130	140	150	160	170	180
m919.pep	YFTPWQVAGNSLAGTVTGYEYEPVLKGDDRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA					
a919	YFTPWQVAGNSLAGTVTGYEYEPVLKGDDRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA					
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL					
a919	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
a919	DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	310	320	330	340	350	360
m919.pep	KLGQTSMOGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
a919	KLGQTSMOGIKAYMQQNPRORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA					
	370	380	390	400	410	420
m919.pep	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
a919	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGA AAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaaagtgg acatcatCCC
501 CTTGCgccaa GGCTTtttga aAgcGAGTGT CGAATAcaaa gccgAttctc
551 CCGATcaaAG CCTGTGccga AAACaggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTA EY OPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YOPTFWSKKK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAI I
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

g920/m920

```

g920.pep          10          20          30
                  PMQLVTEKGKENMIQRGTYNQYRSNRPVK
m920              GGEYLKADLGYGFEPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGTYNQYRSNRPVK
                  40          50          60          70          80          90

g920.pep          40          50          60          70          80          90
                  DGSYLVTAEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
m920              DGSYLVIAEYQPTFWSKKKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
                  100         110         120         130         140         150

g920.pep          100         110         120         130         140         150
                  KPVGQNLEIVPLDNPADIHVGXRFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHKTEA
m920              KPVGQNLEIVPLDNPANIHVGERFKVRVLFERGEPLPNATVTATFDGFDTSDRSKTHXXEA
                  160         170         180         190         200         210

g920.pep          160         170         180         190         200
                  QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTLTTFQIAHSHHX
m920              QAFSDSTDDKGEVDIIIXLRQGFWKANVEHKTDFPDQSVCKQANYSTLTTFQIGHSHHX
                  220         230         240         250         260

```

```

a920.seq
1    TGAAAGAAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCGCATC
51   CGCCCCACGC  CACCGCGTCT  GGGTCGAAAC  CGCCACACAG  CACGGCGGCG
101  AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AAATTTCCCGA  ACTCGAACC
151  ATCGCCAAAG  ACCGCTTGCA  CATCTTCAGC  AAAACCATGC  AGCTGGTTAC
201  CGAAAAAGGC  AAGGAAAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251  ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA
301  TATCAGCCTA  CTTTCTGGTC  AAAAAACAAA  GCAGGCTGGA  AACAGGCGGG
351  CATCAAAACA  ATGCCCTGAG  CAAGCTATTG  CGAACAAAGC  CGAATGTTCT
401  GCAAAAACAT  CGTCAACGTC  GGACACGAAA  CGCGGGACAC  CGCCATCATC
451  ACCAAACCGG  TCGGACAAAA  CTTGGAAATC  GTCCCGCTGG  ACAATCCCGC
501  CAACATTCAC  GTAGGCGAAC  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551  AACCGTTCGC  CAATGCCACC  GTTACCGCCA  CCTTTGACGG  CTTCGACACC
601  AGCGACCGCA  GCAAAACGCA  CAAAACGAA  CCAACAGGCT  TCTCCGACAC
651  CACAGACGAC  AAAGGCGAAG  TGGACATCAT  CCCCTTGCGC  CAAGGCTTCT
701  GGAAGCCCAA  TGTCGAACAC  AAAGCCGACT  TCCCCGATCA  AAGCGTGTGC
751  CAAAAACAGG  CGAACTACTC  GACTTTAACC  TTCCAAATCG  GCCATTGCA
801  CCATTAA

```

a920.ppep

1	<u>*KKTLTLLAV</u>	<u>SALFAASAH</u>	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRLHIFS	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNL EI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD T
201	SDRSKTHKE	EAQFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	QKQANYSTLT	FQIGHSHH*			

BNSDOCID: <WO__9957280A2_| >

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	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
a920	XKKTLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXHEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQANYSTLTFQIGHSHHX					
a920	KADFPDQSVQCQKQANYSTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGcccAAAG ACCgccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCC
401 GTAAAAACAT TGTCACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTTT
701 GGAAAGCGAG TGTCAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGEFFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDTDDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 KQQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACAG CACGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEFFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 KQQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

m920-1.pep	10	20	30	40	50	60
	MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920-1.pep	70	80	90	100	110	120
	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
m920-1.pep	130	140	150	160	170	180
	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920-1.pep	190	200	210	220	230	240
	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTDDKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
m920-1.pep	250	260	269			
	KTDFFDQSVCKQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep

```

1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

```

m920-1/a920 98.9% identity in 267 aa overlap

```

      10      20      30      40      50      60
m920-1.pep  MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a920        XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90     100     110     120
m920-1.pep  KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a920        KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m920-1.pep  MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a920        MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep  FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a920        FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep  KTDFFPDQSVCKQKQANYSTLTFQIGHSHHX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a920        KADFFPDQSVCKQKQANYSTLTFQIGHSHHX
      250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatccccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTGCA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCGG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSADV SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```


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251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSALD SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSALDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSADVDSQGEINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	: :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATGACGGA AATCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSALD SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

1326

	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTTGTG GACGATGAAG TCGGGAAGG GGATTTTCC CAGGCGGAAT
251  GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301  ATGCACCGAC CCTCCACATC GCGTCCGTGG TATgtgttcc gCacggGAAa
351  ttcGGgcagg gcgaaAtttc ACggcgcGCG Caggttttat GcggaaAacc
401  gcgcgggttat cgatgatgtg gcgCAAAAat acggcgtGCC TGCCGAGCTT
451  ATCGTGCGCA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701  ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751  gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA CgggcggTAA
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CAggcAATCA
851  TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901  ggcacatccc ccggggaaaC GCTCGCAGAT GATGAAAAGg cgGTTTTGTT
951  CAAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTG GGCTTGAACA
1001  ATTTTATAC GGTATGGCAG TACAACCACA GCCGATGTA TGTAACGgcg
1051  gtcaggGACA TTGCCAATTC GCTCGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDfs QAEWQDFFDK AAYKADIVKI
101  MHRPSTSRPW YVFRtGNsGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151  IVAIIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFOK ELVELLKLAK
201  EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251  ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGEKTAI TRTVADLKAY
301  GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMVYTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101  CCCCCGCGC GGTTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAT TTGACGCGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251  ATTTTTCCTG GCGGAAATG CAGGATTTT TTGACAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAATT CGGGCAAGGC GAAATTTCCG GCGCGCGGCC
401  GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451  GCGGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501  CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551  GCTTTGATTA CCCCCGCCG GCCGGTTTT TCAAAAAGA ATTGGTCGAG

```

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```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACCGGGC GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1  MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

```

m922.pep      10      20      30      40      50      60
                MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP
g922           10      20      30      40      50
                MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAA-----AVP

m922.pep      70      80      90      100     110     120
                VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
g922           60      70      80      90     100     110
                VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR

m922.pep     130     140     150     160     170     180
                TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL
g922          120     130     140     150     160     170
                TGNSGRAKFHGAARRFYAENRAVIDDVAQKYGVPaelivaiIGIETNYGKNTGSFRVADAL

m922.pep     190     200     210     220     230     240
                ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
g922          180     190     200     210     220     230
                ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY

m922.pep     250     260     270     280     290     300
                DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV
g922          240     250     260     270     280     290
                DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV

m922.pep     310     320     330     340     350     360
                ADLKAYGIIPGEELADDEKAVL FKL ETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
g922          310     320     330     340     350     360
                ADLKAYGIIPGETLADDEKAVL FKL ETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI

```

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	300	310	320	330	340	350
		370				
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCGG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTCCGCG ACGGGAAATT CGGGCAAGGC GAAATTTCCG GCGCGCGGCC
401 GGTTTTATGC GGAAACCGCG GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTT TCCAAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GGCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GGCGGGAATA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAAC CGCACCCGCG GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GSKILVSATL APGADVQAI GEKALTTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKESRPAFDAAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHWRTGGKMLVSATLAPGADVQAIIGEKALTRTV
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANANYMKQHWRTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAACACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRITVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GORRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRITVSGNV
101 LATLILIIYS LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923 . pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923 . pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALGCGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923 . pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923 . seq	1	ATGAAGCGGC	AGGCTTTCTT	CAAACGTATG	GCGTGTGCGG	CATTTCTGTC
	51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTTAC	GCAATATTGT
	101	CCCTCTATGC	GTTTGCACTT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
	151	GGAAAACGCC	GCATTCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCCG
	201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAACCGG
	251	CGAAAAGCG	TTTTGTTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
	301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTTAA	ACCAGTACGG
	351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
	401	ACCAAGTGAA	TCGGTTCCTG	ACTATTTGTA	CTGTCTGCGG	CTTCGTCGCC
	451	TTGTCTGAT	TTTTGTTAAT	CCACTAT.AT	TATTTTGTCC	CGCCTGAATT
	501	TTTCGTAAAA	CTCGGGCAGA	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923 . pep	1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
	51	GKRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFVV	LFRLTVSGNV
	101	LATLILIIYS	LNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
	151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923 . pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923 . pep	LLPALGCGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923 . pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRRTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggT TA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTCACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTCACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTAATTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGE					
	: : : : :					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
	: : : : :					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
	: : : : :					
g925-1	AQAYLDARNALPSNQTYQQRQAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTTAC AGGTAAGGAA GAATCTATGC TTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
		: : :		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGEESLLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90


```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYLDARNALPSNQTYYQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYRDARNALPSNQTYYQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

g926.seq (partial)

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTCTA CCGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

g926.pep (partial)

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

m926.seq

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

m926.pep

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQTEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQSAEELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCROWGASPNVATE

```

m926 ||:||||||| |||||:|:|:| :|
WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq

```

1   ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTG CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGACTGT CCGCAGAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

```

a926.pep

```

1   MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLNI RLVFTEIGMPS ETETQEQQAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKNVYQESAELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKNVYQESAELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQEQQARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

```

1   atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51  CAGCCCcgca GCcgatTcaa accaTCCGTC CGGACAAaAT GCCCCGCGCA
101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTegtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTgtgttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCAGGCC GCACCCTACA

```

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgc
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAActCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAACCGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTQSE HPGTSVSIQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTVPVFENG GRXPPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAT GCCCCGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAAGAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGA AAAA
701 CGAAGCCAAC TACGTCAGCr AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

```

          10      20      30      40      50      60
g927.pep  MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD
          |||||  |||||  |||||  |||||  |||||  |||||
m927       MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

          70      80      90     100     110     120
g927.pep  HLFVGTQSEHPGTSVSIQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK
          ||:  |||||  |||||  |||||  |||||  |||||
m927       PLFIKTYQSEHPGTSVSIQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90     100     110     120

          130     140     150     160     170
g927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA
          |||||  |||||  |||||  |||||  |||||
m927       GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA
          130     140     150     160     170     180

```

1336

```
      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||:||||||||||||||||||||||||||||||||||||||||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
      240
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```
a927.seq
  1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAA  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```
a927.pep
  1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*
```

m927/a927 99.2% identity in 242 aa overlap

```
      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:||||||||||||||||||||||||||||||||||||||||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:||||||||||||||||||||||||||||||||||||||||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:||||||||||||||||||||||||||||||||||||||||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:||||||||||||||||||||||||||||||||||||||||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240
```

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGTT TTGGCACTGC CCGTACcga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTGTGTT
351 TATCGCCGTT TTTGGAAGAA AAacgctggg CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCcgat TATGCagtcg attgCcggCA GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
551 tcaattTCA TTCaaTCCC atttcgctcg ctAtggctat taCTGcaact
601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
651 tttcgcgtCTT Tcttggggggg cgTGGGcggtg ggcaatGGCT Gtccccggcg
701 ttatcgcctt TtctgTTATG CCTTGATTTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCTgttCAA TTTGCCAAAG ACCGTCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTtaAATA Aactcggact gattaaatGG TTCTCCGGAG TGTGGCGGA
1101 Aagtgtcggc GGTtTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTta TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGATATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL AIAAVLCAV LALPVPDGVK PQAWTLLAMP VGVIAAIIGK
51  VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNVAV FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMPASTTAH
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCGATGCCGT TGGGCGCGCT GTCGATTATT CCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTGTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

```

451  GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501  CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551  TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601  GCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651  TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701  TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTTwyT GTATCCGCCT
751  GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801  GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851  GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901  CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951  GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAATGG TTCTCCGGAG TGTGCGCGGA
1101 AAGTGTGGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTTTCGCT GCTGCCGTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGCG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCAV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLVPP
251 EIKETPNVAV FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTA
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCAV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK VMPLGALSII					
m929	MKLGFKPIPLAIAAVLCAV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK AMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRG L LKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRG L LKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSNP ISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNAVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTTGGCGGA
1101 AAGTGTGCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTGCGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101  SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151  GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201  APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251  EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301  HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351  FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401  ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451  GYTTMGEWWK AGFIMSVVNE LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
a929	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
a929	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
a929	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
a929	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
a929	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
a929	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
a929	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
a929	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929

WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```
1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAATGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```
1 MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNP AEIRM QODIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWWLEGEHHA
101 RFQFALKRAL RETGFOAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```
1 GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51 AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCGTAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAAG
201 ACGTATTGCA GCATTCCAAA ACAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAATTTTG
551 ACGCCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGC TTCAACCGCC TGTGTATATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGAAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACCC ACAGGTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTATTTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```
1 GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51 LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTP FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGO IKLGGNLHYD
```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAAC GAAGTGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTT CCACCCGCTC GAACGATCTG
601 TTGAATCTGT GTGATTGGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTG GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAAT TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAAT AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAATGGGA CATGGGCATT CAATCAAAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAACCTG ACTGTACAAC GGCGTAAAC TCGGGTGTGG
1201 TTGGCAGAAC TTTCCACAAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCTGCTA ACATCGCAAG
1451 ACAAACCTGG TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGTTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACCGGGGCA GATAAAGCTT GCGGCAAC TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTTTCA GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLPLSYLPN IRLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAGF NKFPTRSNL
201 LNLRLDLEQL ENLKRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHKKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHOAVSG LSEVVDYNGK
351 SYNTDFGNR LLYRDAKRKT YLGVKLWMRE TKSYYDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGKY WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

```
90      100      110      120      130      140
m930-1.pep AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI
g930-1.pep                               GKCLHAGDINQIMSLAQNALIGRGYTTTRI
                                         10      20      30

150      160      170      180      190      200
m930-1.pep LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAGFQNKFPTRSNLNLRLDLE
g930-1.pep LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAGFQNKFPTRSNLNLRLDLE
                                         40      50      60      70      80      90

210      220      230      240      250      260
m930-1.pep QGLENLKRLEPTAEADLQIVPEGEPEPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG
||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

1343

```

g930-1.pep  QGLENLKLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270
m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALRAPEEAFEGGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTGWLAEELSHKEYIGRSTADFKLKYKHGTGMKDALRAPEEAFEGGTSRMKI
              280      290      300      310      320      330
m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVRGFDGEMSLPAER
              340      350      360      370      380      390
m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450
m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWSGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWTGFGVGYSTX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACCG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCC TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

1	ATGAAACCCA	AATTCAAAAC	CGTTTTAAC	GCGCTGCTTT	TGGCGGTTTC
51	CCTGCCGTCT	ATGGCGGCAA	CCCATGTTTT	GATGGAAACC	GATATGGGCA
101	ATATCCGTTT	GGTTTTGGAC	GAATCCAAAG	CCCCCAAAC	CGTTGCTAAT
151	TTCTGTGCGT	ATGCCCGAAA	AGGCTTTTAC	GACGACACCG	TTTTTCACCG
201	CGTTATCGAC	GGTTTTGTTA	TCCAGGGCGG	TGGATTGACC	GAGGACTTGG
251	CACAAAAGGC	AGCGATAAAG	GCGGTGCCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACCG	CCGGCACCAT	CGCCATGGCG	CGGACGACAG	CCCCCGATTG
351	CGCCACCAGC	CAATTCTTTA	TCAATCTGGC	GGACcA.kCT	TCGCTCGACT
401	ACAAAACCGG	ACAATACGGC	TATACCGTTT	TCGGCAGGGT	CGAAAGCGGC
451	ATGAACACCG	TTTCCAAAAT	CGCCCGCGTC	AAAACCGCCA	CGCGCGGCTT
501	TTATCAAAAC	GTACCCGTAC	AGCCCGTCAA	AATCCGTGCG	GTTGTTGTGCG
551	GGCAGTAA				

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```

1  MKPKFKTVLI  ALLLAVSLPS  MAATHVLMET  DMGNIRLVLD  ESKAPKTVAN
51  FVRYARKGFY  DDTVFHRVID  GFVIQGGGLT  EDLAQKASDK  AVANESGNGL
101 KNTAGTIAMA  RTTAPDSATS  QFFINLADXX  SLDYKNGQYG  YTVFGRVESG
151 MNTVSKIARV  KTATRGFYQN  VPVQPVKIRR  VVVGO*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
g931.pep		MKPKFKTVLTALLLAVSLPSMAATRVL	METDMGNIRLVL	DESKASKTVANFVRYARKGFY			
m931		MKPKFKTVLTALLLAVSLPSMAATHVL	METDMGNIRLVL	DESKAPKTVANFVRYARKGFY			
		10	20	30	40	50	60
		70	80	90	100	110	120
g931.pep		DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
		: :		: :		:	: :
m931		DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
		70	80	90	100	110	120
		130	140	150	160	170	180
g931.pep		QFFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRFGFYQNPVPQPVKIRR					
m931		QFFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRFGFYQNPVPQPVKIRR					
		130	140	150	160	170	180
g931.pep	VVVGQX						
m931	VVVGQX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

1	ATGAAACCCA	AATTCAAAC	CGTTTTAACC	GCGCTGCTTT	TGGCGGTTTC
51	CCTGCCGTCT	ATGGCGGCAA	CCCATGTTTT	GATGAAACC	GATATGGGCA
101	ATATCCGTTT	GGTTTTGGAC	GAATCCAAAG	CACCCAAAAC	CGTTGCCAAT
151	TTCGTGCGCT	ATGCCCGAAA	AGGCTTTTAC	GACAATACGA	TTTTTCACCG
201	CGTCATCGGC	GGCTTCGTTA	TCCAAGGCGG	CGGATTGACC	GAGGACTTGG
251	CACAAAGGCG	AAGCGATAAG	GCCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACTG	TCGGCACCAT	CGCCATTGCG	CGGACGGCCG	ATCCGGATTG
351	CGCCACCAGC	CAATTCTTTA	TCAATCTGGT	GGACAATGAT	TCGCTCAACT
401	ACAAAACCGG	ACAATACGGC	TATACCGTTT	TCGGCAGGGT	CGAAAGCGGG

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451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS OFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	OFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	OFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVGQX					
a931	VVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTTC CACTCACCGC

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```

51  CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTTCAGCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCGCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACGAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAa9g
551 cggtaaaCCC GGCGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1  MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQOGFEHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1  ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51  ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GCGCGGCGCG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAATTCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGACAGCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTtnt GCATTGTGTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRRAVYL RPIDRKLAAA KPGRRGGRRV YRQAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep                                10      20      30
                                      RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
g934      MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
              10      20      30      40      50      60

m934.pep      40      50      60      70      80      90
      PAEAQANGNNGQPVTKXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
g934      PAQAQANGNNGQPVTKRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQAGKQIHTGGQPR
              70      80      90      100     110     120

              100     110     120     130     140     150

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCC CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACGGAAG CTGGCTGTGT CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAATTTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCGTC GCCCGCGCGC CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCGCGGTTT CGGCAGAAGG
551 CGGTAATATC GGCCTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTCCT AAGAGTTTGA TGTCGGGATG GCAATTCTGA

```

a934.pap

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	GQPVTX*RRR	AVYLRPIDRK	LAAAKPGRRG
101	GRRVYRQAG	KQIHTGRQPR	QSRPRACR	LPSVRTSQCA	HQQGFHAQP
151	PCKTTGGAGA	ALPPDNAPAR	QLFPPRHARF	RQKAVNPACQ	CRLKGFQTAF
201	<u>LYLLGTLLCC</u>	<u>RLIFRRHFVS</u>	<u>KSLMSGWQF*</u>		

```

m934.pep                                10      20      30
                                         RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                         |||||
a934      MKKIIASALIATFALAACQDDAQRLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
              10      20      30      40      50      60

              40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
              |||||
a934      PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
              70      80      90      100     110     120

              100     110     120     130     140     150
m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPCKTTGGAXAALPPDNAPXRQLPPPRYARF
              |||||
a934      QSRRPARACRLPSVRTSQCAHQQGFEHAQPCKTTGGAGAALPPDNAPARQLPPPRHARF
              130     140     150     160     170     180

              160     170     180     190     200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
              ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934      RQKAVNPACQCRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
              190     200     210     220     230

```

BNSDOCID: <WO 9957280A2 | >

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```
601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCCGGGCGGA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AATAAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCGGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GGCGCAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTGC
1501 GCGGATTGGC GGTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```
a935.pep
1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAEF
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*
```

m935/a935 98.8% identity in 505 aa overlap

```
10 20 30 40 50 60
m935.pep MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV
|||||
a935 MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV
10 20 30 40 50 60

70 80 90 100 110 120
m935.pep DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
|||||
a935 DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
70 80 90 100 110 120

130 140 150 160 170 180
m935.pep AEAVARYRELHGENAADERILDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF
|||||
a935 AEAVARYRELHGENAADERILDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF
130 140 150 160 170 180

190 200 210 220 230 240
m935.pep RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
|||||
a935 RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
190 200 210 220 230 240

250 260 270 280 290 300
m935.pep LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
|||
a935 LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
250 260 270 280 290 300
```